```
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                 gb_htg8:*
gb_htg9:*
gb_htg10:*
gb_htg11:*
                                                                                 gb_htg12:*
gb_htg13:*
gb_htg13:*
gb_htg14:*
                                                                                                           gb_in3:*
gb_htg15:*
gb_htg16:*
gb_htg17:*
                                                                                                                                                                                      gb_htg18:*
gb_htg19:*
         em_htg2:*
em_htg3:*
                                                                                                                                                     em_htg5:*
em_htg6:*
                                 gb_p13:*
gb_pr5:*
                                                                                                                                                                                                                                                                                                                                                                                       Query
Match I
                                                                                                                                           62:
63:
64:
65:
66:
                                                                                                                                                                                                                                                                                                                                                                                                Score
                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                 ; Search time 1334.93 Seconds (without alignments) 1927.840 Million cell updates/sec
                                                                                                   1 cccgggaactccatgtggcc.....aatgcaattcatttggatcc 1442
                                                                                                                                                                              1945680
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                            972840 seqs, 892348106 residues
                                                 9, 2000, 20:47:27
                                                                                                                                                                                                                         summaries
                                 OM nucleic - nucleic search, using sw model
                                                                                                                   OLIGO_NUC
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                       Post-processing: Listing first 45
                                                                                  US-09-214-679-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 em_vi:*
gb_htg1:*
gb_htg2:*
gb_in1:*
gb_in2:*
                                                                                                                                                                                                                                                                                                                                                                                              em_hum2: *
em_in: *
em_om: *
em_or: *
em_ov: *
em_pat: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ba2:*
hum3:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gb_pr4:*
gb_htg3:*
gb_htg4:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gb_htg5:*
gb_htg6:*
                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 1000000
                                                                                                                                                                                                                                                                                                                                                                                       em_hum1:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      em_hum4:*
                                                                                                                                                                                                                                                                                                                            gb_pr2:*
gb_pr3:*
gb_ro:*
gb_sts:*
gb_sy:*
gb_un:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                        em_pl:*
em_ro:*
em_sts:*
                                                                                                                                                                                                                                        em_sy:*
em_un:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              em_ba1:*
                                                                                                                                                                                                                                                                  gb_om:*
gb_ov:*
gb_pat:*
gb_ph:*
gb_pl:*
gb_pl2:*
gb_pl2:*
                                                  September
                                                                                                                                                                                                                                                                                                                                    Title:
Perfect score:
                                                                                                                    Scoring table:
```

Database :

Word size

Searched:

Sequence:

Run on:

em\_hum6:\*

em\_htg7:

A72152 Sequence 1
A0057459 Glardia i
AF018076 Rickettsia
083457 Rickettsia
083457 Rickettsia
08345 Thai Lick t
08347 Rickettsia
AF120019 Rickettsia
AF120020 Rickettsia
083436 Rickettsia
083436 Rickettsia
083446 Rickettsia
083448 Rickettsia

RCU83443 RCU83448 RCU83453

3182 3182 3182 3182

A69475 Sequence 1

Description

Length DB

~

|taggaccagggagtattacctatctgccggtacgtgcgcctggaggccgcctgtttat coatcaccaccatcaaagtcgatttgatcaagaactggcagctttcctggccacgaat egtggagaataacatatgaaatggttggaagaatccattatggccaaacgcggtgttgg gccgggcgtaaaccggtaacgcatcacctgacggaagaaatgcaaaaagagtttcatta rectacatgettetgagteaatgeggeaaagtgeggetggggeaacatggtegaeeecaa

Db 61 CCGCACACGCTGTGCGGTAATGGATAAAGGCCTGGTTGTAGAAACGCTGACCCAACAAC 120 Oy 121 agctctctgatgatcttttaatgcgtcgtcatctggtaactaaacgctataaatt 180	Oy 181 acgiggagaataacatatgaaatggtiggaagaatccattaiggccaaacgcggtgtigg 240 	Oy 241 tgccgggcgtaaaccggtaacgcatcacctgacggaagaaatgcaaaaagagtttcatta 300 	Oy 301 caccattggccttattccacaccgtcctgaccatcgaacccggtgaccggattattgt 360	Oy 361 cgacactcgagatgctttgaaggtgctatcaattcggaacaggatattccgagccagtt 420	Qy 421 gctaaaaatgcctttctcaacccacaaacggaccgatcatggtcaatggcggggga 480	<pre>Qy 481 aggtgatgtgtctatatcgaatccatgttgccccgcgcgcqttgatccctacgg 540                                      </pre>	Oy 541 catctgcgccatgattccgcattttggcggactgaccgggaccgacc	Oy 601 caatgatccgctgccagaaaagtgcgcatgattaaactcgacagtgaaaaggtctactg 660	Oy 661 gagcaaacgccatacgcttccctataaaccccatattggcaccttgagcgtatcgccaga 720	Oy 721 aattgactcaatcaattcactgacgccagacaatcacgggggaatatggatgtgccgga 780 	Oy 781 tataggaccagggagtattacctatctgccggtacgtgcgcctggaggccgcctgtttat 840	Oy 841 tggtgatgcccatgcttgtcagggtgatggtgagatttgcgggaccgcagtagagtttgc 900	Oy 901 ctcaatcaccaccatcaaagtcgatttgatcaagaactggcagctttcctggccacgaat 960	Qy 961 ggagaatgccgaaaatattatgagtattggcagtgcacgtccgctggaggatgcgacgcg 1020 	Oy 1021 aattgcatatcgcgacttaatttactggctggtagaagactttggcttcgaacaatggga 1080 	Qy 1081 tgcctacatgcttctgagtcaatgcggcaaagtgcggctgggcaacatggtcgaccccaa 1140	Oy 1141 atacaccgttggcgcgatgctgaacaaaacctgttagtta
	о п	<u> </u>		<del>о</del> п	<del>о</del> н	- A	<del></del>	<del>о</del> п	<u>о</u> п	о <u>п</u>		о <sub>п</sub>	о п	<u> </u>	<u>о</u> п	<u>,</u>	
Db 1141 ATACACCGTTGGCGCGATGCTGAACAAAACCTGTTAGTTA	Oy 1261 cagctaaagcaggtgcatatggggccagatacacccatcaatattggtttactttactcc 1320 	Qy 1321 ttcagcggagtgacggcgcacaagagttgtcacaatggcgcggagcaacccaggctatt 1380 	Qy 1381 gccgaaattaatcaaaatggcggcatcaacggcagaccactcaatgcaattcatttggat 1440 	Qy 1441 cc 1442 	RESULT 2 A72152 A72152 1442 by DAY 11-MAY-1000	ITION Sequence 1 from Patent W09801568. SION A72152 ON A72152.1 GI:4808107	SOURCE Klebsiella oxytoca. ORGANISM Klebsiella oxytoca Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;	to 1442) Naughton, A., Robins, I. T.	AL Patent: WO 9801568-A 15-JAN-1998; LONZA AG (CA)	Source	/db_xref="taxon:571"  CDS 197. 1183  /**Codon_start=1 /**rearc1 +=h.h.o.=1	/product="AwIDASE" /protein_id="CAB42722.1" /db_xref="G1:48081108" /t-a_10:4:a_10:48081108"	LT GIBS ALOUNG WINDERS IMPARKY VIANTEE PROMINE HIT I LOFT STEV  LT I EPOEDRI I VOTTRAPECA I INSECONTE SOLLKWPF LINFONGP INWNGARKGDVLAVY  I ESMLPRGVDPYGICAMI PHFGGLIGTDLTAMLNDPLPEKVRMIKLDSEKVYWSKRHT  LYKPHIGTLEVSVPEPIDSI INSLINGINGON POPI GROGSTYLLPVRAFGGRLEFTGDA  UN CHOCKET CHANNERS AT TIME LITPON FROM AN AND AND AND AND AND AND AND AND AND	ACCOUNT 385 a 350 c 370 g 337 t. ORIGIN	Query Match Best Local Similarity 100.0%; Score 1442; DB 5; Length 1442; Best Local Similarity 100.0%; Pred. No. 0; Matches 1442. Conservative O: Mismatches	cccgggaactccatgtggccgtgatcttggtcgagcaggatattgcgatgatccagcggg 60	61 ccgcacagcgctgtgcggtaatggataaagcctggttgtagaaacgctgacccaacacacac

ò Db g

g δλ

q δŏ

δý

```
RMU83439 3167 bp DNA BCT 10-SEP-1998
Rickettsia mongolotimonae rOmpA (ompA) gene, partial cds.
229 CCAAACGCGGTGTTGGTGCC 210
                                                                                                                                                     U83439.1 GI:1778884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                                         RESULT 4
RMU83439/c
                                                                                                               DEFINITION
                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
                                                                                                                               ACCESSION
VERSION
                                                                                                                                                                                                                                                                                      AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                               MEDLINE
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                    KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGIN
                                                                                             LOCUS
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dubitted (18-APR-2000) Josephine Bay Paul Center for Comparative Molecular Biology and Evolution, Marine Biological Laboratory, 7 MBL Street, Woods Hole, MA 02543-1015, USA Sequencing reads that have not been assembled into configs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC057459 1100 bp DNA HTG 18-APR-2000
Giardia intestinalis clone MJ2849 strain WB-C6, LOW-PASS SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for Comparative
                                                                                         tgaacattacccggatgtagatcggggtaatgtgtaagttcaaacaatcgctatttttaa 1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Glardia. 1 (bases 1 to 1100)
Morfison, H.G., McArthur, A.G., Nixon, J., Eakin, N.Q., Kim, U., Crocker, M.C., Hinkle, G., Holder, M.E. and Sogin, M.L. Giardia: a model for ancient eukaryotic genome analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Morrison, H.G., McArthur, A.G., Nixon, J., Eakin, N.Q., Kim, U., Crocker, M.C., Hinkle, G., Holder, M.E. and Sogin, M.L. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 20; DB 77; Length 1100;
Pred. No. 6;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1100: contig of 1100 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .lluu
/organism="Giardia intestinalis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:5741"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        222 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 1.4%; Scr
Best Local Similarity 100.0%; P.
Matches 20; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="MJ2849"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC057459
AC057459.1 G1:7594157
HTG: HTG2_PHASEO.
Glardla intestinalis.
Glardla intestinalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ccaaacgcggtgttggtgcc 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 1100)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      299 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SAMPLING.
                                                                                                                                                                                                                                                                                                                                                   1441 CC 1442
                                                                                                                                                                                                                                                                                                                       1441 cc 1442
                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
AC057459/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
               1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                        1321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
JOURNAL
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             225
                                                                                                                                                                    1321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMMENT
```

ōλ

```
ALLIYNAVITTDDVALGABOAT VARANDA VARANDA KANADA VARANDA 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Raoult, D., Fournier, P.-E. and Roux, V.
Direct Submission
Submitted (31-DEC-1996) Faculte de Medecine, Unite des Rickettsies,
CNRS EP 30054, 27 bd Jean Moulin, Cedex 5, Marseille, France
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ILNVNTKLLTAYHLTIGTVAEINIGAGNIFAIDASAGDVTILNAQDIHFRALDSTLLL.
SNLTGVGVNNILLAADLVAPGADEGTVVFNGGVNGLNIGSNVAGTARNIGDGGGNKFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="ITLHAGGSLDANNIDFGARSTLEFNGGGGIPYYFKGAIANGNNA
                                                                                                                                                  Rickettsiaceae, Rickettsieae, Rickettsia.
1 (bases 1 to 3167)
Fournier, P. E., Roux, V. and Raoult, D.
Phylogenetic analysis of spotted fever group rickettsiae by study of the outer surface protein rompA
Int. J. Syst. Bacteriol. 48 Pt 3, 839-849 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                            Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.4%; Score 20; DB 2; Length 3167;
100.0%; Pred. No. 6.6;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Rickettsia mongolotimonae"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAKYKMMEYGINYDTNIGSKYFAQQ"
513 c 666 g 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="rOmpA"
/protein_id="AAC35175.1"
/db_xref="G1:1778885"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:45261"
Rickettsia mongolotimonae. Rickettsia mongolotimonae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=3
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="HA-91"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1373 aggetattgeegaaattaat 1392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1603 AGCTATTGCCGAAATTAAT 1584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="ompA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="ompA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 3167)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <1. .>3167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
AF018076/c
```

```
Rickettsia sibirica.

Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsiaee; Rickettsia.

1 (bases 1 to 3176)

S Fournier, P. E., Roux, V. and Raoult, D.
Phylogenetic analysis of spotted fever group rickettsiae by study of the outer surface protein romph.

Int. J. Syst. Bacteriol. 48 Pt 3, 839-849 (1998)

B8404549

Raoult, D., Fournier, P. -E. and Roux, V.
Direct Submission

Location, Codex 5, Marseille, France
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KENALLIYNAYTI DDVALEGION LINNADETSSTRANGYIO ONATYTI DANNO
NLNIPAGNIOPAHADAQLI LONSSGNDRTITLGANIDPNDDBGIVILNSYTAGRKIT
TAGGRIFGGAHKLQTIVKGGDGGTGTFRYRNIVLDITGQLELGATTANVULFRD
AVQLTQTGNIGGFLADANGTTLANGYTGTTRTRNIVLDITGGLELGATTANVULFRD
AVQLTQTGNIGGFLATANGYTTLANGTTLALBAHVNITGGRALITUTGANNRYN
MGGSVGGVVGTAANSVGDITTAGATSFASSVNARGTAKLGGTTSFAHTFTNGAYTLA
KGSITSFAKNITATSFYANSATINFGNSLAFNSNITGSGTALTLGGTSFAHTFTNGAYTLA
RGSITSFAKNITATSFYANSATINFGNSLAFNSNITGSGSTLTLGGGTGFTTT
AANNOVANSNITSSNITALNANREVENSTALLANDRANGTANDANTYTGGGFT
ANDRANIKSSLELMEDAPNGSDARQAFNNGLAMPHLANDTANTGAYTA
AANNOVASNISSNITALNARREDKVGPVSSGDEDMDAKFGANTISFVGRATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KMCNSISGYKSDTTGGTIGFDGFVSDDLVLGLAYTRADTDIKLKIIKTADKNKVESNI
YSLYGLYSVPYENLFYEAIASYSDIRIGSKSRRVIATTLETVGYQTANGKYKSESYTG
QLMAGYTYMMPENINLTPLVGLRYSTIKDKGYKETGTTYQNLTVKGKNYNTFDGLLGA
KSSNINVNEIVLTPELYAMVDYAFKNKVSAIDARLQGMTAPLPTNSFKQSKTSFDVG
VGYPAKYKMMEYGINTDLYLAMVOYAFKRKVSAIDARLQGMTAPLPTNSFKQSKTSFDVG
VGYPAKYKMMEYGINT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NNAILNVNTKLLTAYHLTIGTVAEINIGAGNIFAIDASAGDYTILNAODIHFRALDST
LVLSNLTGVGVNNILLAADLVAPGAGEGTVIFNGGVNGLHIGSNVAGTARNIGDGGGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="ITLHAGGSLDANNIDFGARSTLEFNGPLDGGGIPYYFKGAIANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTU83456 3176 bp DNA BCT 10-SEP-1998
Thai tick typhus rickettsia rOmpA (ompA) gene, partial cds.
U83456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thai tick typhus rickettsia.
Thai tick typhus rickettsia
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
1 (bases 1 to 3176)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.4%; Score 20; DB 2; Length 3176;
100.0%; Pred. No. 6.6;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    1. .3176
/organism="Rickettsia sibirica"
/strain="246"
/db_xref="taxon:35793"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="AAC35191.1"
/db_xref="G1:1778905"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="rOmpA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1373 aggetattgeegaaattaat 1392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1612 AGGCTATTGCCGAAATTAAT 1593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="ompA"
<1. .>3176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="ompA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      U83456.1 GI:1778906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 1.4
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTU83456/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                             ORGANISM
                                                                                                                                     AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                               REFERENCE
                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                            MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GNOTILINVWIKELTATHETECTIVAELINGAGEMENTELINAQDINGERALDSA
LVESNITGATORITEAADLVAPGADECTVVPINGGVNGLINGSWAGTRRINGSAG
LVESNITGYGVNUILLAADLVAPGADECTVVPINGGVNGLINGSWAGTRRINGDGGGN
KFWILSI YNAVI TIDDVNILEGIQNULINDANDFTSSTAFNAGTIQITKDATYTIDANNG
NLNI PAGNIQFAHADAQLILQNSSGNDRTITIGANIDPDNDDEGIY ILNSVTAGKKLTI
IAGGKMFGGAHKLOTIVKGAGNCGARGTTFWTTNI VLDITGGLELGATTASVULFND
AVOLTOTGNIGGFLDFNAKNGTYTLNNVNVAGTVONTGTNNGTLI VLGASNLNRVN
GIAMLKVGAGNTI IAKGGNTATLANNVNTGTNTGSTNRTGGANTTGSTNRTGGALKLPM
NSGSVGVVGTAANSVGDITTAGATGFASSVNAKGTATLGGTTSFANIFTGAVTLA
KGSITSFANVYTATGSTNAGATGFASSVNAKGTATLGGTTSFANIFTGAVTLA
KGSITSFAKNYTATGFORAKGGGTTTNGROLLANNSVITTGGGOLKLPM
SAGTKRPTROCAAKSGGNILIKSGSTLDLSGVSTTALLVTATRIDMNNISSPTKTVVI
SAGTAGGLKPPRENVKITINNDNRPVDFTCDASTLTLFAEDIAADVIDEDFAPGGPL
ANIPNAANIKKSLELMEDAPNGSDRQAFTNPCGANTPLQGADATTHLMQDVVKPSDTI
AAVNNQVVASNISSNITGATIGFTLANRAMNKGPVSGCDEDMDARFGGANTGSNIT
KMONSISSNITGATIGFTLANRAMNKGPVATRANTTANTGCHNTKTGDKNKYESNIT
                                                                                                                                                                                                                                                                                                                                                                                 930-300.

2 (bases 1 to 3176)

Roux,V., Thiers,B. and Raoult,D.

Direct Submission

Submitted (11-AUG-1997) Faculte de Medecine, Unite des Rickettsies,

CNRS UPRES-A 6020, 27, bd Jean Moulin, Marseille 13385, France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YSVYGLYNVPYENLEVEALASYSDNK IRSKSRRVIATTLETVGYQTANGKYKSESYTG
QLMAGYTYMMPENINLTPLAGLRYSTIKDKGYKETGTTYQNLTVKGKNYNNFDGLLGA
KVSSNINVNEIVLTPELYAMVDYAFKNKVSAIDARLQGMTAPLPTNSFKQSKTSFDVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="AaC83454.1"
/db_xref="GI:3982571"
/translation="ITLQAGGSLAANNIDFGAGSTLDFNGPLGGGNAIPYYFKGAIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                            Stenos, J., Roux, V., Walker, D. and Raoult, D.
Rickettsia hone; sp. nov., the aetiological agent of Flinders Island spotted fever in Australia
Int. J. Syst. Bacteriol. 48, 1399-1404 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-SEP-1998
        08-DEC-1998
                                                                                                                                                        Rickettsia honei
ascteria: proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
1 (bases 1 to 3 176)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 3176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RSU83455 3176 bp DNA BCT 10
Rickettsia sibirica rOmpA (OmpA) gene, partial cds.
U83455
U83455.1 GI:1778904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
  AF018076 3176 bp DNA BCT
Rickettsia honei rOmpA (ompA) gene, partial cds.
AF018076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.4%; Score 20; DB 2;
100.0%; Pred. No. 6.6;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VGVTAKHKMMEYGINYDTNIGSKYFAQQ"
523 c 677 g 913 t

    .3176
    /organism="Rickettsia honei"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="RB"
/db_xref="taxon:37816"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /transl_table=11
/product="rOmpA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1373 aggctattgccgaaattaat 1392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1612 AGGCTATTGCCGAAATTAAT 1593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=3
                                                                                 AF018076.1 GI:3982570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="ompA"
<1. .>3176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <ī. .>3176
/gene="ompA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <1. .>3176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 1.4
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                     honei.
                                                                                                                                     Rickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
RSU83455/C
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
                             DEFINITION
ACCESSION
                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
                                                                              VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                           MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGIN
```

; 0

Gaps

;

à a

```
/codon_start=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1373 aggetattgeegaaattaat 1392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DD 1615 AGGCTATTGCCGAAATTAAT 1596
                                                                                                                                                                                                                                                                                                                                                                         /dene="ompA"
                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="ompA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rickettsia sp. DnS28.
                            2 (bases 1 to 3179)
                                                                                                                                                                                                                                                                                                                                                                                               <1. .>3179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
nes 20, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF120018S2/c
                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                      AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
TITLE
JOURNAL
                                                                                                                   JOURNAL
                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                                                                                                                            gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KEYWORDS
SEGMENT
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LVISNITGOGONNILLIAADLAAPGADEGTVERGGONGLNIGGSNAGGARTIN NATED TO THE ACTUAL AND THE ACTUAL ACTUAL TO THE ACTUAL ACTUAL ACTUAL TO THE ACTUAL ACTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SAETAGGLK PTPKENVK ITINNDNRFVDFTFDASTLILLFAEDIAADVIDEDFARGED-
ANIPPRANIRKSLELMEDAPNGSDARQAFNNFGLMTPLQEADATTHIMQDVVRPSDFI
AAVNDVVASNI SSNITALNARMDKVQAGNKGPVSGDEDMDARFGAMISPFVSNATQ
KMCNSISGYKSDTTGGTIGFDGFYSDDLALGLAYTRADTDIRLKNNRTGDKNKVESNIT
YSVYGLYNVPYENLFVEAIASYSDNKIRSKSRRVIATTLETVGYQTANGKYKSESYTG
ALMAGYTYMPRENIALFAGLIKSTIKKOKYKETGTTYQNLTVKGKNYNNFDGLIGA
KVSSNINNNETVLTBELYAWYDYAFNNKVSAIDARLQGMTAPLPTNSFKQSKTSFDVG
VGVTAKHKMMEYGINYDFNIGSKYFAQQ"
                                                                                                                                                               Course 1 to 3176)
Raoult, D., Fournier, P.-E. and Roux, V.
Direct Submission
Submitted (31-DEC-1996) Faculte de Medecine, Unite des Rickettsies,
CNRS EP J0054, 27 bd Jean Moulin, Cedex 5, Marseille, France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAC35192.1"
/db_xref="G1:1778907"
/translation="ITLQAGGSLAANNIDFGAGSTLDFNGPLGGGNAIPYYFKGAIAN
GNNAILNVNYKLTAYHSTIGTVAEINIGAGNLLEIDASAGDVTILNAQDINFRALDSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
Fournier, P.E., Roux, V. and Raoult, D.
Phylogenetic analysis of spotted fever group rickettsiae by study
of the outer surface protein rOmpA
Int. J. Syst. Bacteriol. 48 Pt 3, 839-849 (1998)
98404549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rickettsia montanensis:
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsia.
1 (bases 1 to 3179)
Fournier, P.E., Roux, V. and Raoult, D.
Phylogenetic analysis of spotted fever group rickettsiae by study of the outer surface protein rompA
Int. J. Syst. Bacteriol. 48 Pt 3, 839-849 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.4%; Score 20; DB 2; Length 3176; 100.0%; Pred. No. 6.6; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RMU83447 3179 bp DNA BCT
Rickettsia montana rOmpA (ompA) gene, partial cds.
U83447.1 GI:1778890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                      /organism="Tha! tick typhus rickettsia"/strain="TT-118"
/db_xref="taxon:45259"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="rompA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1373 aggetattgeegaaattaat 1392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1612 AGGCTATTGCCGAAATTAAT 1593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rickettsia montanensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="ompA"
<1. .>3176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="ompA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .>3176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 1.45
Best Local Similarity 100.0
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1063
                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RMU83447/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
TITLE
                                                                                                                                               MEDLINE
REFERENCE
                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
                         AUTHORS
                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEYWORDS
                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                      TITLE
                                                                                                                                                                                                                                            TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
```

.

```
NONLINPAGNICE THE CONTROLL TO THE CONTROLL THE CONTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rickettsia sp. DnS28
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsiaee; Rickettsia; spotted fever group.

1 (bases 1 to 3182)
Rydkina,E., Roux,V., Fetisova,N., Rudakov,N., Gafarova,M.,
Tarasevich,T. and Raoult,D.
Detection of New Spotted Fever Group Rickettsiae in Ticks Collected in the Former USSR
Raoult_D., Fournier,P.-B. and Roux,V.

Direct Submission

Submitted (31-DEC-1996) Faculte de Medecine, Unite des Rickettsies,
CNRS EP J0054, 27 bd Jean Moulin, Cedex 5, Marseille, France
Location/Qualifiers
1. 3179
/organism="Rickettsia montanensis"
/strain="M5/6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STLMLYNLTGVGVKNILLAADLVAPGADEGCVVFNGGMNGLNIGSNVAGTARNIGDGG
GDKFNNLFIYNVVKVTDDVNLEGIKNVFIGNDADFTSSTACNAGTIQINNATYAIDAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IAAVNNQVVASNISSNITALNARMDEVQAVNKCPVSSGDEDMDVKFGAMÏSPFVGNAT
QKMCNNISGYKSDTTGGTIGFDGLVSDDLALGLAYTRADTDIKLKNNKMGDKNKVESN
IYSLYGLYSVPYENLFVEAIASYSDNKIRSKSRRVIATALETVGYQTANGKYKSEGYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="ITLQAGGSLAANNIDFGVGSTLEFNGPLDGGGDIHYHFKGAIA
NGNNATLNVNTKSLTAYHSTIGPVAEINIGADSFFTIDASAGDVTILNAQDINFRAQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GQLMAGYTYMMPENINLFPLAGLRYSTIKDKGYKETGTTYQNLTVVĞKNYNTFDGLLG
ARVSSNINVNEIVLTPELYAMYDYAFKNKVSAIDARLQGMAAPLPTNSFKQSKTSFDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (14-JAN-1999) Unite Des Rickettsies, Faculte De Medecine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.4%; Score 20; DB 2; Length 3179;
100.0%; Pred. No. 6.6;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF12001852 3182 bp DNA BCT 1
STGKettsia sp. DnS28 OmpA (ompA) gene, partial cds.
AF120019.1 GI:6979178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 3182)
Rydkina, E., Roux, V., Raoult, D. and Tarasevich, I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GVGVTAKHKMMEYGINYDTNIGSKYFAQQ"
516 c 682 g 926 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAC35183.1"
/db_xref="G1:1778891"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:33991"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="rompA
```

```
Rickettsia sp. RpA4.

Rickettsia sp. RpA4.

Rickettsia sp. RpA4

Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Bickettsiaceae; Rickettsieae; Rickettsia; spotted fever group.

1 (bases 1 to 3182)

Rydkina,E., Roux,V., Fetisova,N., Rudakov,N., Gafarova,M.,
Tarasevich,I. and Raoult,D.

Detection of New Spotted Fever Group Rickettsiae in Ticks Collected in the Former USSR
                                                                                                                                                                                                                                                           /translation="ITLQAGGSLAANNIDFGVGSTLEFNGPLDGGGNTIPYYFKGAIA
NGNNAILNVNTKSLTAYHSTIGTVAEINIGAGNLFAIDASAGDVTILNAQDINFGAPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 3182)
Rydkina.E., Roux, V., Raoult, D. and Tarasevich, I.
Bydkina.E., Roux, P., Raoult, D. and Tarasevich, I.
Direct Submission
Submitted (14-JAN-1999) Unite des Rickettsies, Faculte de Medecine,
27 boulevard Jean Moulin, Marseille 13385, France
Location/Qualifiers
1. 3182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.4%; Score 20; DB 2; Length 3182;
100.0%; Pred. No. 6.6;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rickettsia sp. RpA4 OmpA (ompA) gene, partial cds. AF120023
AF120023.1 GI:6979188
                                                                     /note="isolated in the former USSR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Rickettsia sp. RpA4"
                                                                                                                                                       /note="outer membrane protein"

    .3182
    /organism="Rickettsia sp.

                                                                                                                                                                                                                           /protein_id="AAF34348.1"
/db_xref="G1:6979184"
                                 /strain="DnS14"
/db_xref="taxon:114648"
                                                                                                                                                                                         /transl_table=11
/product="OmpA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1373 aggetattgeegaaattaat 1392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1618 AGGCTATTGCCGAAATTAAT 1599
                                                                                                                                                                         /codon_start=3
                                                                                                   /gene="ompA"
<1. .>3182
                                                                                                                                       /gene="ompA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3182 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 1.49
Best Local Similarity 100.0
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF120022S2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
AF120022S2/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
JOURNAL
                                                                                       gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                     CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEGMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δλ
                                                                                                                                                                                                                                                                                    Rickettsia sp. DnS14.
Rickettsia sp. DnS14
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsiaee; Rickettsia; spotted fever group.
[1] (bases 1 to 3182)
Rydkina,E., Roux,V., Fetisova,N., Rudakov,N., Gafarova,M.,
Tarasevich,I. and Raoult,D.
Detection of New Spotted Fever Group Rickettsiae in Ticks Collected in the Former USSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGQLMAGYTYMMPENINLTPLAGLRYSTIKDKGYKETGTTYQNLTVÄGKNYNTFDCLL.
GAKVSSNINVNEIVLTPELYAMVDYAFKNKVPAIDARLQGMTAPLPTNSFKQSKTSFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tropies 1 to 3182)
Rydkina, E., Roux, V., Raoult, D. and Tarasevich, I.
Direct Submission
Submitted (14-JAN-1999) Unite des Rickettsies, Faculte de Medecine, 27 Boulevard Jean Moulin, Marseille 13385, France
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.4%; Score 20; DB 2; Length 3182;
100.0%; Pred. No. 6.6;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF120020S1 3182 bp DNA BCT 1
Rickettsia sp. DnS14 OmpA (ompA) gene, partial cds.
27 Boulevard Jean Moulin, Marseille 13385, France
Location/Qualifiers
                                              /organism="Rickettsia sp. DnS28"
/strain="DnS28"
/db.xref="taxon:114649"
/nore="isolated in the former USSR"
                                                                                                                                                                                       /note="outer membrance protein"
/codon_start=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VGVGVTAKHKMMEYGINYDTNIGSKYFAQQ"
                                                                                                                                                                                                                                                      /protein_id="AAF34347.1"
/db_xref="G1:6979180"
                                                                                                                                                                                                                         /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1373 aggctattgccgaaattaat 1392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1618 AGGCTATTGCCGAAATTAAT 1599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF120020
AF120020.1 GI:6979182
                                                                                                                                     /gene="ompA"
                                                                                                                                                                      /gene="ompA"
                                                                                                                                                  . .>3182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 of 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
AF12002081/c
LOCUS AE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
VERSION
                                                                                                                     gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEYWORDS
SEGMENT
SOURCE
                                                                                                                                                       CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
```

g δį

ö

```
/codon_start=3
/transl_table=11
/gene="ompA'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Int. J. S. 98404549
                                                                                                                                                                                                                                                                                                                                                                                                         1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
RCU83440/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
               CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                      /protein_id="AAF34351.1"
/db_xref="GI:6979190"
/translation="ITLQAGGSLAANNIDFCVGSTLEFNGPLDGGGNTIPYYFKGAIA
                                                                                                                                                                                                                                                                                                                                                                                                    TQKMCNNĪSGYKSDTTGGTIGFDGLVSDDLVLGLAYTRADTDIKLKNNKTGDKNKVES
TISTJEGYRVPYENLEVEALAFYSDNKIISKSKERVLAYALETGYGYONGKYKSESY
TGQLAMAGYTYWAMPRINILTPLAGLRYSTIKONGY KETGTTQONLTVKGKNYNTEDGLL
GAKVSSNINVNEIVLTPELYAMVDYAFKNKVPAIDARLQGMTAPLPTNSFKQSKTSFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Raoult, D., Fournier, P.-E. and Roux, V.
Direct Submission
Submitted (31-DEC-1996) Faculte de Medecine, Unite des Rickettsies,
CNRS EP J0054, 27 bd Jean Moulin, Cedex 5, Marseille, France
Location/Qualifiers
1. 3182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rickettsia africae
Bacteria, Proteobacteria, alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsiae.
1 (bases 1 to 3182)
Pournier, P.E., Roux, V. and Raoult, D.
Phylogenetic analysis of spotted fever group rickettsiae by study of the outer surface protein rompA
Int. J. Syst. Bacteriol. 48 Pt 3, 839-849 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 1.4%; Score 20; DB 2; Length 3182; Best Local Similarity 100.0%; Pred. No. 6.6; Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RAU83436 3182 bp DNA BCT
Rickettsia africae rOmpA (ompA) gene, partial cds.
          /db_xref="taxon:114650"
/note="isolated in the former USSR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               VGVGVTAKHKMMEYGINYDTNIGSKYFAQQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Rickettsia africae"
/strain="ESF 2500-1"
/db_xref="taxon:35788"
1. 3182
                                                                                                   /note="outer membrane protein"
                                                                                                                                   /transl_table=11
/product="OmpA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=3
                                                        /gene="ompA"
<1. .>3182
                                                                                       /gene="ompA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U83436.1 GI:1778870
                                          .>3182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rickettsia africae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U83436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
RAU83436/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
TITLE
                                           gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                       CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     õ
```

,\*

```
/ULEANS 1 & LOI: 17 / 108 / 1
/ULEANS 1 & LOI: 17 / 108 / 1
/ULEANS 1 & LOI: 17 / 108 / 1
/ULEANS 1 & LOI: 17 / 108 / 1
/ULEANS 1 & LOI: 17 / 108 / 1
/ULEANS 1 & LOI: 17 / 108 / 1
SALVISNAGORINGARIA DES AGDYT ILNAQDIHERALD
SALVISNAGUGGORINGARIA DES AGDYT AGDENAGTARIGOGG
GNEKPYLLIYNAYT ITDDUNES GONDET I LGANI DPDNDDEG I VILNSYTAGEK
LITAGGEMEGGHEGOTILONS GONDET I TLGANI DPDNDDEG I VILNSYTAGEK
LITAGGEMEGGHEKOTI VEKGAGDOT GATET FONT THIN MID ITGGLEGATANIVULE
KDAYOLTOTORI GGYLDEPRAKNOGTTENTTANT THE NOGTANIK TOTORING
VOGTAMLEK VGAGNYT I AKGONYK I GEI OGTOTNT LILPAHFNIL TGSINKT GGOLLKIN
FMIGGSV GGYVOTTANISV GES SONNAKTAT LGST SEHET FHYGAYT
LAKGS I TSPAKNYTANIS FORMAT I REGNIS LARNSYT GSGT STEHET FRYGAYT
LAKGS I TSPAKNYTANIS FORMAT I REGNIS LARNSYT GSGT STEHET FROMOVTYTGTG
PLANIT PNAALK KGLELMARDANG GONNET GLAST LIL FRABLIA ADVID KORPA FOG
PLANIT PNAALK KGLELMARDANG KGPNET GLAST LIL FRABLIA ADVID KORPA FOG
PLANIT PNAALK KGLELMARDANG KGPNEN FOR SCHTLER RODD AADVID CORPAGE
T GOLMAGYT YMMPEN I NITALNARMEN KGPYS SGDEDMDAKFGAMI SPFVGNA
T GOLMAGYT YMMPEN I NITALNARMA KSK SKRYL ATTLET VGCNIS KK SESY
T GOLMAGYT YMMPEN I NIT PLAGLKY STIKOK KT KT TTLET VGCNIS KK SESY
T GOLMAGYT YMMPEN I NIT PLAGLKY STIKOK SK TT TOTOLT V KGKNYNT F DGLL
GAK VSSINNNNEI I ULT PELLARVAN VANN VANN VANN T TTLET V GKNYNT F F DGLL
GAK VSSINNNNEI I ULT PELLARVAN VANN VANN T TTLET V GKNYNT K SESY
T GGLMAGYT YMMPEN I NIT T PLAGN SK T KROK T K TTLET V GKNYNT K SESY
T GGLMAGYT YMMPEN I NIT T PLAGN T SK T K ROO!"

GAK VSSINNNNEI ULL PELLARVAN VANN VANN T F DAGLT K SK T K F T G T T G GAT C ST T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G G T G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Z (bases 1 to 3182)
Raoult,D., Fournier,P.-E. and Roux,V.
Direct Submission
Submitted (31-DEC-1996) Faculte de Medecine, Unite des Rickettsies,
CNRS ET 70054, 27 bd Jean Moulin, Cedex 5, Marseille, France
. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ricketts) access: Rickettsiaee; Rickettsiae.

1 (bases 1 to 3182)
Frounder, P.B., Roux, V. and Raoult, D.
Phylogenetic analysis of spotted fever group rickettsiae by study of the outer surface protein romp.

Int. J. Syst. Bacteriol. 48 Pt 3, 839-849 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 1.4%; Score 20; DB 2; Length 3182; Best Local Similarity 100.0%; Pred. No. 6.6; Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RCU83440 3182 bp DNA BCT
Rickettsia conorii rOmpA (ompA) gene, partial cds.
U83440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .3182
/organism="Rickettsia conorii"
/strain="Indian tick typhus"
/db_xref="taxon:781"
                                                                                               /protein_id="AAC35172.1"
/db_xref="GI:1778871"
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1618 AGGCTATTGCCGAAATTAAT 1599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qy 1373 aggctattgccgaaattaat 1392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="ompA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="ompA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U83440.1 GI:1778874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rickettsia conorii.
Rickettsia conorii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .>3182
```

```
/translation="VTLQAGGSLDANNIDFGARSTLEFNGPLDGGGNAIPYYFKGAIA
NGNNAILNVNTKLLTAYHLTIGTVAEINIGAGNLFAIDASAGDVTILNAQDIHFRALD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Raoult,D., Fournier,P.-E. and Roux,V.
Direct Submission
Submitted (31-DEC-1996) Faculte de Medecine, Unite des Rickettsies,
CNRS EP 37 bd Jean Moulin, Cedex 5, Marseille, France
Location/Qualifiers
                                                                                                                                                                                                                                                                                                    GAKVSSNINVNEIVLTPELYAMVDYAFKNKVSAIDARLQGMTAPLPTNSFKQSKTSFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 3182)
Fournier,P.E., Roux,V. and Raoult,D.
Phylogenetic analysis of spotted fever group rickettsiae by study
of the outer surface protein rOmpA
Int. J. Syst. Bacteriol. 48 Pt 3, 839-849 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rickettsia conorii
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                ..
0
                                                                                                                                                                                                                                                                                                                                                                                            1.4%; Score 20; DB 2; Length 3182;
100.0%; Pred. No. 6.6;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rickettsia conorii rOmpA (ompA) gene, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                    VGVGVTAKHKMMEYGINYDTNIGSKYFAQQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Rickettsia conorii"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="AAC35179.1"
/db_xref="G1:1778877"
/protein_id="AAC35176.1"
/db_xref="GI:1778875"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     db_xref="taxon:781"
                                                                                                                                                                                                                                                                                                                                 673 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="rompA'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1618 AGGCTATTGCCGAAATTAAT 1599
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1373 aggctattgccgaaattaat 1392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="Ml"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="ompA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="ompA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3182 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     U83443
U83443.1 GI:1778876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 3182)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rickettsia conorii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . .>3182
                                                                                                                                                                                                                                                                                                                                                                                                                             20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .3182
                                                                                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Int. J. S
98404549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RCU83443
                                                                                                                                                                                                                                                                                                                                 1065
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
RCU83443/c
                                                                                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCUS
```

δ g

```
LAKGSITSERAKUVTATIONEN TINEGNELARUS NITGSGTTLITGANQUTTITUTORY TO THE CAST TERRAKUVTATORY OF A THE CAST TO THE CAST TH
GNKFNTILIYNAVTITDDVNLEGIQNVLINNNADFTSSTAFNAGTIQINDATYTIDAN
NGNLMIPAGNIKFAHADAQLILQNSSGNDRTITLGANIDPDNDDEGIVLINSVTAGKK
LITAGGKTFGGAHKLQAIVFKGEGDFGTAGTFFNTHNIVLDITTGLEEGATTANVLF
KDAVGTGGFLDFANKNGTVLINNNVNVAGTVKNTGGTNNGTLIVLGASNLNR
VNGIAALKVGAGNYTAKGGNY IGELQGTGNYTLTLPAHFKLIGSINKTGGALKLN
FMNGGSVSGVVGTAANSVGDITTAGATSFASSVNAKGTATLGGTTSFAHFFNTGAYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SALVLSNLTGVGVNNILLAADLVAPGVDEGTVVFDGGVNGLNIGSNVAGÄARNIGDVG
GNFRWTLLIYAAVTITDDVNLEGIONVLINNAADFTSSTAFNAGTIOINDATYTIDAN
NGNLNIPAGNIKFAHADAQLILQNSSONDRTITLGANIDPDNDDEGIVILNSYTAGKK
LITAGGRIFGGAHKLQAIVFKGEGDFGTAGTFFNTTNIYUDJTGQLELGATPANVULF
KDAVQLTQTGNIGGFLDFNAKHGTVTLNNVNVAGTVKNTGGTNNGTLIVLGASNLNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="VTLQAGGSLDANNIDFGARSTLEFNGPLDGGGNAIPYYFKGAIA
NGNNAILNVNTKLLTAYHLTIGTVAEINIGAGNLFAIDASAGDVTILNAQDIHFRALD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unite des Rickettsies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; alpha subdivision; Rickettsiales; Rickettsiaceae: Rickettsiaeae; Rickettsiae.

1 (bases 1 to 3182)
Fournier,P.E., Roux,V. and Raoult,D.
Phylogenetic analysis of spotted fever group rickettsiae by study of the outer surface protein rOmpA
Int. J. Syst. Bacteriol. 48 Pt 3, 839-849 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Raoult, D., Fournier, P.-E. and Roux, V.
Direct Submission
Submitted (31-DEC-1996) Faculte de Medecine, Unite des Ricket
CNRS EP 30054, 27 bd Jean Moulin, Cedex 5, Marseille, France
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.4%; Score 20; DB 2; Length 3182; 100.0%; Pred. No. 6.6; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RCU83448 3182 bp DNA BCT Rickettsia conorii rOmpA (ompA) gene, partial cds.

    3182
    /organism="Rickettsia conorii"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="AAC35184.1"
/db_xref="G1:1778879"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="Moroccan"
/db_xref="taxon:781"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=3
/transl_table=11
/product="rOmpA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1373 aggctattgccgaaattaat 1392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1618 AGGCTATTGCCGAAATTAAT 1599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="ompA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="ompA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   U83448.1 GI:1778878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 3182)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .>3182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rickettsia conorii. Rickettsia conorii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98404549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
RCU83448/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŏ
```

```
VNGIAMLKVGAGNYTIAKGGNVKIGEIQGTGTNTLTLPAHFKLTGSINKTGGQALKLN
FNNGGSVSGVVGTAANSVGDITTAGATSFASSVNAKGTATLGGTTSFAHTFTNTGAVT
LAKGSITSFRANVTATSFVANSATINFGNSLARNNITGSGTLTLGAOVYTYTGTGS
FTDTLTLANTFDGAAKSGGNILIKSGSTLDLSGVSNLALVYTANNFDMNISPDTKYT
VISAETAGGIKPTPKENVKITINNNRFVDFTFDASTLTLFAEDIAAGVIDEDFAGG
PLANIPMAANIKKSLELEMEDAPNGSDARQAFNRTGLMFTLAGADATHLMQDVKRFSD
TAAVNNQVVASNISSNITALNARMDKVQAGNKGPVSGDEDMDAKFGANISPFVGNA
TAAVNOVASNISSNITALNARMDKVQAGNKGPVSGDEDMDAKFGANISPFVGNA
TORMCNSLSGYKEDTTGGTIGFDCFVSDDLVLGLAYTRADTDIKLKNNKTGDKNKVES
NIYSLYGLYSVPYENLFVBAIASYSDNKIRSKSRRVIATLETVGYQTANGKYKSESY
TGQLMAGYTYM MAENIUTTPLAGIRKYSTIKDSYKRGTYQULTVKGKRYNTFDGLL
GAKVSSNINVNETVLTPELXAMSKYSTIKDKSKRETTYQULTVKGKRYNTFDGLL
GAKVSSNINVNETVLTPELXAMSKYSTIKDKSKREDPTNSFKQSKTSFD
VGVGVTAAKHKMMEYGINTDYNIGSKYFAQO"

1062 a 512 c 675 g 933 t
```

0;

.; 0

> Search completed: September 9, 2000, 22:01:05 Job time: 4418 sec

000000

00000

New

```
Tri:fluoro-2-hydroxy-2-methyl-propionic acid enantiomer preparation
- by stereoselective hydrolysis of corresponding racemic amide using
- by stereoselective hydrolysis of corresponding racemic amide using
- by stereoselective hydrolysis of corresponding racemic amide using
- microorganism or derived enzyme, used as drug intermediate

Claim 7a; Page 32-34; 68pp; German.

This DNA sequence encodes a R-specific amidohydrolase isolated from
the sequence encodes a R-specific amidohydrolase is used in a process for preparing
(R)-isoforms of 3.3-trifluoro-2-hydroxy-2-methyl propionamide which
is cheaper than prior art optical resolution of the racemate using
dimethoxy strychnine or (S)-(-)- alpha -methylbenzylamine.
Sequence 1442 BP; 385 A; 350 C; 370 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 acgtggagaataacatatgaaatggttggaagaatccattatggccaaacgcggtgttgg 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 ccgcacagcgctgtgcggtaatggataaaggcctggttgtagaaacgctgacccaacaac 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 agctctctgatgatcttttaatgcgtcgtcatctggctctgtaactaaacgctataaatt 180
                                                   EE520-3. N.
                                                                               EE528-1. N
EEE69-1. N
EE528-2. N
                                                                      EEE37-2.
                                          EE520-2.
                                                                                                                 EEE69-2.
                               EE520-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 cccgggaactccatgtggccgtgatcctggtcgagcaggatattgcgatgatccagcggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1442;
 16-JUN-1998 (first entry)
K. oxytoca R-specific amidohydrolase genomic DNA.
K. systedic amidohydrolase; hydrolysis; racemate; nitrogen 3,3.3-trifluoro-2-hydroxy-2-methyl propionamide; isoform; Klebsiella oxytoca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                           (LONZ ) LONZA AG.
Brieden W, Naughton A, Robins K, Shaw N, Tinschert A,
                                                                                                                                                                                                                                                                                                                /note= "R-specific amidohydrolase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 1442; 100.0%; Pred. No. 0;
                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                        Location/Qualifiers
197. .1183
        Q21221
Q21258
Q21326
Q21327
Q21328
Q21328
Q21058
Q21058
Q21061
Q21061
Q21061
                                                                                                                                                                                                V10449 standard; DNA; 1442 BP
                                                                                                                                                                                                                                                                                            /*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 1442; Conservative
                                                                                                                                                                                                                                                                                                     /product=
                                                                                                                                                                                                                                                                                                                                    15-JAN-1998.
10-JUL-1997; E03670.
03-MAR-1997; CH-000500.
10-JUL-1996; CH-001723.
                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 98-101063/09.
P-PSDB; W40263.
                                                                                                                                                                                                                                                                                                                           WO9801568-A2.
                                                                                                                                                                                                                                                                                                                                                                                                Zimmermann T;
1100110011001100110011001100110011001100110011001100110011001100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                           V10449;
RESULT
                                                                                                                                                                                       V10449
                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                    ; Search time 66.13 Seconds (without alignments) 5455.572 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lacS gene C-termin
lacS gene C-termin
Primer 2. Stable i
Primer 3. Stable i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New a New a New a New a New a New a New a
                                                                                                                                                                                                                                                                                                                                                                                                                     K. oxytoca R-speci
Nad B gene encodin
                                                                                                                                                                                                                                                                                                                                                                                                                                          K. oxytoca R-speci
The nadA nucleotid
The nadA nucleotid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HIV-1 breakthrough
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIV-1 breakthrough
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Borrelia burgdorfe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               faeca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Borrelia burgdorfe
Borrelia burgdorfe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      faeca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus aur
Sequence encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      faeca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human haematopoiet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enterococcus faeca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         faeca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   promoter,
                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                   1 cccgggaactccatgtggcc.....aatgcaattcatttggatcc 1442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EE505-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PND EE322-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EE229-2.
                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCOAOMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PND
PND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PND
                                                                                                                                                                                                                              623170
       version 4.5
- 2000 Compugen Ltd.
                                                                                                                                                                                                                               parameters:
                                                                                                                                                                                     311585 seqs, 125096042 residues
                                                                     9, 2000, 21:26:38
                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                 - nucleic search, using sw model
                                                                                                                                                                                                                                                                                Post-processing: Listing first 45 summaries
                                                                                                                                                        OLIGO_NUC
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q51468
Q51469
V20812
V00522
V00521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X20225
X20306
X28141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X12948
V74544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q21239
Q21236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q21238
Q21240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 049600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X20275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X20274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X13059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       021237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N60194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               021267
                                                                                                                                                                                                                            Total number of hits satisfying chosen
         GenCore
Copyright (c) 1993
                                                                                                              US-09-214-679-1
                                                                                                                                                                                                                                                                                                     N_Geneseq_36:*
                                                                                                                                                                                                                                                                                                                                                                                                Match Length DB
                                                                                                                                                                                                                                                  seq length: 0
seq length: 1000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6444
7227
7227
9813
102
102
102
102
102
102
103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1501
1512
1883
2019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4312
                                                                      September
                                                                                                                                                                                                                                                                                                                                                                                                                    100.0
                                                                                                                                                                                                                                                                                                                                                                                      Query
                                                                                                                                                                                                                                                                                                                                                                                                                                Perfect score:
                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                 Score
                                                                                                                                                                                                          Word size :
                                                                                                                                                                                                                                                   Minimum DB
Maximum DB
                                                 OM nucleic
                                                                                                                                                                                                                                                                                                     Database :
                                                                                                                                   Sequence:
                                                                                                                                                                                      Searched:
                                                                      Run on:
                                                                                                                                                                                                                                                                                                                                                                                      Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Š.
```

0 0 0,0 0

ö

Gaps 9

```
q
                                                                                                                                                                                                      ŏ
    240
            300
                                   360
                                           420
                   300
                         caccattggcccttattccacacccgtcctgaccatcgaacccggtgaccggattattgt 360
                                            480
                                                                   480
                                                                           540
                                                                                   540
                                                                                          009
                                                                                                                                                                                                         1020
                                                                                                                                                                                                                1020
                                                                                                                                                                                                                     9
                                                                                                          099
                                                                                                                  9
                                                                                                                                                                                                                                                        1200
                                                                                                                          720
                                                                                                                                  720
                                                                                                                                          780
                                                                                                                                                 780
                                                                                                                                                      841 tggtgatgcccatgcttgtcagggtgatggtgagatttgcgggaccgcagtagagttgc 900
                                                                                                                                                                                 900
                                                                                                                                                                                         960
ACGTGGAGAATAACATATGAAATGGTTGGAAGAATCCATTATGGCCAAACGCGGTGTTGG
            tgccgggcgtaaaccggtaacgcatcacctgacggaagaaatgcaaaaagagtttcatta
                            cgacactcgagatgcttttgaaggtgctatcaattcggaacaggatattccgagccagtt
                                                                       gotaaaaatgocotttotcaacccacaaaacggaccgatcatggtcaatggcgggggaaa
                                                                                      aattgactcaatcaattcactgacgccagacaatcacggcgggaatatggatgtgccgga
                                                                                                                                                                                     181
                        301
                                        361
                                                361
                                                        421
                                                                                       541
                                                                                              541
                                                                                                       601
                                                                                                              601
                                                                                                                              661
                                                                                                                      199
                                                                                                                                      721
                                                                                                                                                                                             901
                                                                                                                                                                                     901
                                                                                                                                                                                                                     1021
                                                                                                                                                                                                                             1021
                                                                                                                                                                                                      961
                                                                                                                                                                                                                                     1081
                                                                                                                                                                                                                                            1081
                                                                                                                                                                                                                                                     1141
                                                                                                                                                                                                                                                            1141
                                                                                                                                                                                                                                                                            1201
                                                                                                                                                                                                             961
                                                                                                                                                                                                                                                                    1201
g
        ò
               Dp
                       οy
                               g
                                              Dp
                                       δy
                                                       à
                                                             g
                                                                      Ω
                                                                             Op
                                                                                             go '
                                                                                      δy
                                                                                                      δ
                                                                                                             Dp
                                                                                                                      QY,
                                                                                                                            qq
                                                                                                                                    ò
                                                                                                                                            엄
                                                                                                                                                     å
                                                                                                                                                            qq
                                                                                                                                                                             g
                                                                                                                                                                     οy
                                                                                                                                                                                     δ
                                                                                                                                                                                            q
                                                                                                                                                                                                     ò
                                                                                                                                                                                                            g
                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                           g
```

```
ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oxidase.

Claim 7; Page 4-5; 24pp; German.

Between this 3* end sequence and the 5* end sequence of N80036 are
ca. 200 bp not represented in the specification.

The nad A sequence (N80035) encoding a polypeptide with the biological activity of quinollinic acid synthase, together with nad B encoding a polypeptide with the biological activity of L appartate is inserted into polypeptide with the biological activity of L appartate is inserted into pharmaceuticals and plant protection agents.

Sequence 1263 BP; 307 A; 324 C; 344 G; 284 T; 4 Others;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ses contg.
aspartate
  1380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
V10449/C
ID V10449 standard; DNA; 1442 BP.
AC V10449:
DT 16-JUN-1998 (first entry)
DE K. oxytoca R-specific amidohydrolase genomic DNA.
KW R-specific amidohydrolase; hydrolysis; racemate; nitrogen source; KW 3,3,3-trifluoro-2-hydroxy-2-methyl propionamide; isoform; ds.
FT Key Location/Qualifiers
FT CDS 197. il83
FT /*tag= a //product= //product= //note= "R-specific amidohydrolase"
FT //note= "R-specific amidohydrolase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                      - have DNA sequences
ic synthase and L asp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ž
                                                                                                                                                                                                                                                                                                                                                                                                             B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kunz
                                                                                                                                                                                                                                                                                                                                                                                                             nad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 1263; 7.4;
                                                                                                                                                                                                                                                                                                                           N82205;
12-NOV-1990 (first entry)
Nad B quee encoding L aspartate 3' end.
Nad B quee encoding L aspartate oxidase; nad A; nad Quinolinic acid synthase; L aspartate oxidase; nad A; nad B plant protection agent; ss.
Escharichia coli (K12C600).
D B8-AGG-1988.
C 04-FEB-1987; 703255.
R 04-FEB-1987; 703255.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Holtmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (RUTG) Rurgerswerke AG.
Laufer A, Gassen HG, Flachmann R, Hoke H, Holtma.
Stadelhofer J, Seifert J;
WPI, 88-2537/34.
Plasmids coded for quinolinic acid synthesis - h
genetic information for synthesis of quinolinic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.2%; Scur
100.0%; Pre
                                                                                                                                                                                                                                                                                                                    BP.
                                                                                                                                                                                                                                                                                      N82205/c
ID N82205 standard; DNA; 1263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  459 tcatggtcaatggcgcgg 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 1.2'
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            594 TCATGGTCAATGGCGCGG
                                                                                                                                                                                           | | |
| 1441 CC 1442
                                                                                                                                                                   1441 cc 1442
                                                                                                                                                                                                                                                                      ~
1321
ò
                                   QΩ
                                                                             ŏ
                                                                                                                    g
                                                                                                                                                                 à
                                                                                                                                                                                                  a
```

 $\sim$ 

```
Discussion by Carman.

To codes for guinolinic acid synthase. Also claimed are nadB which codes for L-aspartate oxidase and genetically transformed microorganisms contg. Pasmids bearing nadA and nadB DNA in a copy ratio of 50:200, 8:50 or 8:200. Isolated chromosomal DNA was digested with HindlI to obtain 6 and 8 kb fragments, which were inserted into PBR322 and cloned in E. coli NK6042 to obtain plasmid pQAB510. This was digested with HindIII and NruI cto obtain a 3.2 kb fragment, which was inserted in pBR322 to produce pQAB 520. This was digested with Spi and NruI to obtain a 2.5 kb fragment, which was inserted into phr234 cc 520. This was digested with Spi and NruI to obtain a 2.5 kb fragment, cc pt and BamHI to give a 2.5 kb fragment, which was inserted into phr234 cc optain pQAB12. This was digested with AluI, ligated with HinciII-cleaved cobtain pQAB12. This was digested with AluI, ligated with HinciII-cleaved cc obtain pQAB12. This was digested with AluI, ligated with HinciII-cleaved cc pUC18 and cloned in E. coli 431 to give pQAA166. This was digested with BamII and PStI to isolate a 1.4 kb insert, which was inserted into PStI cc obtain the nadA-contg. plasmid pQAA16. The BamII and PStI to isolate a 1.4 kb insert, which was inserted into PStI cc Transformation of E. coli w434 to give pQAA166. This was digested with a 50:200 copy ratio, glving quinollinic acid in yields which were ca. 2.6-2.8 times those obtained using w446. The calid swhich were ca. 2.6-2.8 times those obtained using w446. The calid is an intermediate for pharmaceuticals and plant protection agents. Sequence 1724 BP; 408 A; 432 C; 470 G; 414 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 6; 24pp; English.
The sequence is that of a PCR primer which was used in the amplification of a ca. 900 bp long fragment, pBM37, contg. the C-terminal end of lacS from FspI linearised pDP228. The primer introduces a
The nadA nucleotide sequence used in effecting prodn. of quinolinic acid Quinolinic acid production; nadA; nadB; pharmaceutical intermediate; plant protection agent intermediate; quinolinic acid synthase; pBR322; L-aspartate oxidase; Escherichia coli W4546; Escherichia coli NK6042; pQAB10; pQAB520; pQAB333; pHT234; pQAB104; pLG339; Escherichia coli RFI; pQAA12; pUC18; pQAA166; pQA169.
                                                                                                                                                                                                                                                                                                                                                                          using genetically transformed microorganisms contg. nadA and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 1724; 7.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Integral gene expression in food-grade microorganisms - by insertion of a promoter-less gene into an operon in front essential cistron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lacS gene C-terminal fragment PCR primer 2. Polymerase chain reaction; amplification; donor plasmid;
                                                                                                                                                                                                                                                                                            Laufer A, Gassen HG, Flachmann R, Kunz N, Seifert J; WPI; 90-045656/07.
Fermentative prodn. of quinolinic acid -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.2%; Score 18; DB
100.0%; Pred. No. 7.5
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (NEST) SOC PROD NESTLE SA.
Knol J, Marciset O, Mollet B;
WPI; 93-322227/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
Q49599/c
ID Q49599 standard; DNA; 26 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            459 tcatggtcaatggcgcgg 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 1.2
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                         30-JUL-1988; 826041.
30-JUL-1988; DE-826041.
(RUTG) Rutgerswerke Ag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP-105973
                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; p; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-OCT-1993,
31-MAR-1993, 105303,
07-APR-1992, EP-1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    construction; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
EP-564965-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                   nadB genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        049599;
     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           It codes for quinollinic acid synthase. Also claimed are nadb which codes for quinollinic acid synthase. Also claimed microorganisms contging Laspartate oxidase and genetically transformed microorganisms contgiplasmids bearing nada and nadb in a copy ratio of 200:50 or 200:8.

Transformation of E. coli W4546 successively with pQAB 520 and pQAA produced a transformant with a 200:50 copy ratio, giving quinollinic acid in yields which were ca. 7.5-9.7 times those obtained using W4546. The microorganisms give high yields in a reproducible manner. Quinollinic acid is an intermediate for pharmaceuticals and plant protection agents. Sequence 1724 BP; 408 A; 432 C; 470 G; 414 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-JUL-1990 (first entry)
The nadA nucleotide sequence used in effecting prodn. of quinolinic acid Quinolinic acid production; nadA; nadB; pharmaceutical intermediate; plant protection agent intermediate; quinolinic acid synthase; L-aspartate oxidase; Escherichia coli W4546.
                                                                                                                         Trifluoro-2-hydroxy-2-methyl-proplonic acid enantiomer preparation
by stereoselective hydrolysis of corresponding racemic amide using
microorganism or derived enzyme, used as drug intermediate
claim 7a; Page 32-34; 68p; German.
This DNA sequence encodes a R-specific amidohydrolase isolated from
Klebsielha oxytoca strain PRS1 which allows the microorganism to
utilise 3,3,3-trifluoro-2-hydroxy-2-methyl propionamide as its sole
nitrogen source. This amidohydrolase is used in a process for preparing
(R)-isoforms of 3,3,3-trifluoro-2-hydroxy-2-methyl propionamide which
is cheaper than prior art optical resolution of the racemate using
dimethoxy strychnine or (S)-(-)- alpha methylbenzylamine.
Sequence 1442 BP; 385 A; 350 C; 370 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      using genetically transformed microorganisms contg. nadA and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 18; DB 1; Length 1724; Pred. No. 7.5; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.2%; Score 18; DB 1; Length 1442; 00.0%; Pred. No. 7.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                           Brieden W, Naughton A, Robins K, Shaw N, Tinschert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (RUTG) Rutgerswerke Ag.
Laufer A, Gassen HG, Flachmann R, Kunz N;
WPI; 90-045655/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fermentative prodn. of quinolinic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.2°,
100.0%; Pre-
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.08; Pr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          003361/c
ID 003361 standard; DNA; 1724 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
Q03363/c
ID Q03363 standard; DNA; 1724 BP.
AC Q03363;
DT 24-JUL-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            459 tcatggtcaatggcgcgg 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           976 TCATGGTCAATGGCGCGG 959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 CCGCACAGCGCTGTGCGG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 ccgcacagcgctgtgcgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JUL-1988; 826040.
30-JUL-1988; DE-826040.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; p; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                             WPI; 98-101063/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-FEB-1990.
                                                       2immermann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nadB genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
```

Matches

RESULT

Ω

ŏ

ò

Gaps

ö

ō

Matches

ò q ö

```
EP-569604-A.
                                                                                                                                                                                                                                                                                                                                                                            18-NOV-1993
                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                           Primer 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                       051469:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
                                                                                                                                                                                                                                                     RESULT
Q51469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             V20812
      88888888888888
                                                                                                                                                                                               ολ
                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                      ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 6; 24pp; English.

The sequence is that of a PCR primer which was used in the amplification of a ca. 700 bp long fragment, pBM38, contg. the C-terminal end of lacS from FspI linearised pDP228. The PCR amplification was performed as part of the construction of donor plasmids for the integration of the cat gene into the lac operon.

Sequence 26 BP; 14 A; 3 C; 5 G; 4 T;
                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polymerase chain reaction; PCR; primer; amplify; stable; integration; homogenic; heterogenic; Streptococcus thermophilus; restriction site; donor plasmid; artificial; milk product; yohgurt; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                               Integral gene expression in food-grade microorganisms - by insertion of a promoter-less gene into an operon in front of an essential cistron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stable integration of homo., heterogenic or artificial genes integrated streptococcus thermophilus genome - to produce an acidified milk
                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
NdeI site. The PCR amplification was performed as part of construction of donor plasmids for the integration of the
                                                                     Length 26;
                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 26;
                                                                                                                                                                                                                         lacS gene C-terminal fragment PCR primer 3.
Polymerase chain reaction; amplification; donor plasmid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                    Ξ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                    14
                                                                    DB 1;
24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                           1.2%; Scc. 100.0%; Pred. No. 2 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                  3 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 17;
                                  5
C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.08; FIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prod., pref. yoghurt
Example 2; Page 5; 9pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Knol J, Marciset O, Mollet B; WPI; 93-360915/46.
                                                                                                                                                                                                                                                                                                                          Knol J, Marciset O, Mollet B;
WPI; 93-32227/41.
                                                                                                                                                                                   Q49600 standard; DNA; 26 BP.
Q49600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q51468 standard; DNA; 26 BP.
                                                                                                                                                                                                                                                                               13-0CT-1993,
31-MAR-1993; 105303,
07-APR-1992; EP-105973,
(NEST ) SOC PROD NESTLE SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-APR-1992; 105973.
07-APR-1992; EP-105973.
(NEST ) SOC PROD NESTLE SA.
                                                                                                              185 ggagaataacatatgaa 201
                                                                                                                                                                                                            27-APR-1994 (first entry)
                                    4 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185 ggagaataacatatgaa 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-MAY-1994 (first entry)
                       gene into the lac operon.
Sequence 26 BP; 4 A:
                                                                 Query Match 1.2
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 GGAGAATAACATATGAA 20
                                                                                                                         23 GGAGAATAACATATGAA 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.2
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                construction; ss.
                                                                                                                                                                                                                                                                    EP-564965-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EP-569604-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-NOV-1993
                                Šequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Primer 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   051468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q51468/c
                                                                                                                                                                    RESULT
                                                                                                                                                                              049600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                    88888
                                                                                                                                  qq
                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
```

```
Human haematopoletic stem cell growth factor coding sequence. Haematopoletic stem cell growth factor; SCGF; burst-promoting activity; BPA; granulocyte macrophage colony stimulating activity; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polymerase chain reaction, PCR, primer; amplify; stable; integration, homogenic; heterogenic; Streptococcus thermophilus; restriction site; donor plasmid; artificial; milk product; yohgurt; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
The sequences given in 051467-72 are primers which were used in the stable integration of homo- or heterogenic genes into the Streptococcocus thermophilus genome. These plasmids which allowed insertion sites within donor plasmids which allowed insertion of the required genes into the S. thermophilus genome. S. thermophilus transformed in this way may be used in the production of an artificial milk product, especially yohgurt. Integration is stable and follows a strict copy number control of the host genome. The integrated gene may be expressed without the need for direct selection, observable phenotype or adaptation of the growth medium. Sequence 26 BP; 4 A; 5 C; 3 G; 14 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The metal sequences given in 051467-72 are primers which were used in the stable integration of homo- or heterogenic genes into the Strable integration of homo- or heterogenic genes into the Streptococcus thermophilus genome. These plasmids which allowed insertion sites within donor plasmids which allowed insertion of the required genes into the S. thermophilus genome. S. thermophilus transformed in this way may be used in the production of an artificial milk product, especially yohgurt. Integration is stable and follows a strict copy number control of the host genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The integrated gene may be expressed without the need for direct selection, observable phenotype or adaptation of the growth medium. Sequence 26~\mathrm{BP}; 14~\mathrm{A}; 3~\mathrm{C}; 5~\mathrm{G}; 4~\mathrm{T};
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         streptococcus thermophilus genome - to produce an acidified milk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                    1.2%; Score 17; DB 1; Length 26; 100.0%; Pred. No. 24; O: Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Knol J, Marciset O, Mollet B;
WPI; 93-360915/46.
Stable integration of homo-, heterogenic or artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.2%; Score 17;
100.0%; Pred. No.
ive 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              V20812 standard; cDNA to mRNA; 1196 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prod., pref. yoghurt
Example 2; Page 5; 9pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-APR-1992; 105973.
07-APR-1992; EP-105973.
(NEST ) SOC PROD NESTLE SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-MAY-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 ggagaataacatatgaa 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            V20812;
16-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185 ggagaataacatatgaa 201
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 1.2
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 GGAGAATAACATATGAA 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 GGAGAATAACATATGAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q51469 standard; DNA; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
```

ö

Ł

```
X20225
ID X20225 standard; DNA; 1883 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GETH ) GENENTECH INC
Berman PW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JAN-1998.
03-JUL-1997; U09690.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98-101059/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; W37058
                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9801564-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-JUL-1996;
                                                                                                                Seguence
                                                                                                                                                                                                                                                                                                                          V00521;
                                                                                                                                                                                                                                                                                RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
                                                                                                                                                                                                                                                                                               V00521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
 88888888888
                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                             δλ
                                                                                                                                                                                                                                                                          Claim 14; Page 42-44; 85pp; Japanese.

This sequence encodes the human haematopoietic stem cell growth factor (SCGF) of the invention. The polypeptide of the invention is of mammalian origin and has haematopoietic stem cell growth factor SCGF activity, including burst-promoting activity (BPA) and granulocyte macrophage colony stimulating activity (GPA). The products can be used for treatment, diagnosis and analysis of haematopoietic cell disorders and bone marrow inhibition, e.g. by cytotoxic anticancer agents such as 5-fluorouracil. The products can also be used for amplification of haematopoietic cells in vitro, e.g. for use in marrow grafting and gene therapy by insertion of SCGF gene using a suitable therapeutic vector. Sequence 1196 BP; 378 C; 377 G; 181 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
haematopoietic cell disorder; bone marrow inhibition; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Presbb; wav.ou.

Furbul, wav.ou.

Breakthrough strains - useful in providing added protection against HIV not provided by original vaccine

Claim 6; Page 112-114; 193pp; English of the provided by original vaccine

Clone C15.3 encodes a gpl20 envelope polypeptide (see W37059) of a breakthrough isolate of HIV-1 obtained from an individual infected with HIV-1 through high risk activity while participating in phase I or phase 2 trials of MN-rappl20, a candidate recombinant appl20 HIV-1 vaccine. Nucleotide sequences (see V00517-30) for gpl20 polypeptides (see W37054-67) were obtained from 2 clones of each of 7 breakthrough isolates. The envelope glycoprotein genes
                                                                                                                                                                                                                                Haematopoletic stem cell growth factor - useful for, e.g. treatment and diagnosis of haematopoletic cell abnormalities and bone marrow inhibition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-JUL-1998 (first entry)
HIV-1 breakthrough isolate clone C15.3 gpl20 polypeptide DNA.
HIV-1; envelope protein; gpl20; MN-rgpl20; vaccine; AIDS; ss.
Human immunodeficiency virus type 1.
Key
Location/Qualifiers
CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.2%; Score 17; DB 1; Length 1196; 100.0%; Pred. No. 25; 0; Indels iive 0; Mismatches 0; Indels
                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               V00522 standard; DNA; 1501 BP. V00522;
                                                                                                                                                                              (KYOW ) KYOWA HAKKO KOGYO KK.
Hiraoka A, Mio H, Sugimura A;
WPI; 98-179383/16.
                                       140. .877
/*tag= a
1097. .1102
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  964 TTCCTGGCCACGAATGG 980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  946 ttcctggccacgaatgg 962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 1.2
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                          05-MAR-1998.
27-AUG-1997; J02985.
07-JUL-1997; WO-J02349.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag=
                                                                                                                                                 27-AUG-1996; JP-262252
24-MAR-1997; JP-087242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JAN-1998.
03-JUL-1997; U09690.
08-JUL-1996; US-676737
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98-101059/09.
                                                                                                                                                                                                                       P-PSDB: W53245.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; W37059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9801564-A1.
                                                                                             WO9808869-A1
             sapiens
                                                                 polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Berman PW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VÕ0522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
a
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Theraphy was your transplants of the providing added protection against breakthrough strains - useful in providing added protection against breakthrough strains - useful in providing added protection against HIV not provided by original vaccine claim 6; Page 108-110; 193pp; English.

Clone C15.2 encodes a gp120 envelope polypeptide (see W37058) of a breakthrough isolate of HIV-1 obtained from an individual infected with HIV-1 through high risk activity while participating in phase I or phase 2 trials of MNI-rgp120, a candidate recombinant gp120 HIV-1 vaccine. Nucleotide sequences (see V00517-30) for agp120 polypeptides (see W37054-67) were obtained from 2 clones of each of 7 breakthrough isolates. The envelope glycoprotein genes were obtained from proviral DAA using PCR (see V00533-38). All 7 envelope glycoproteins possess sequences typical of subtype (clade) B viruses. The overall homology with MNI-rgp120, is 69-80%. Use of the gp120 polypeptides from one or more of the breakthrough isolates, usually together with MNI-rgp120, can provide protection against HIV strains that are sufficiently different from the vaccine strain (e.g. MNI-rgp120) that the vaccine does not confer protection against those strains.
                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                 (clade)
                          envelope glycoproteins possess sequences typical of subtype (clade by futures. The overall homology with MN-rgp120 is 69-803. Use of the gp120 polypeptides from one or more of the breakthrough isolates, usually together with MN-rgp120, can provide protection against HIV strahms that are sufficiently different from the vaccine strain (e.g. MN-rgp120) that the vaccine does not confer protection against those strains.
   A11 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-JUL-1998 (first entry)
HIV-1 breakthrough isolate clone C15.2 gpl20 polypeptide DNA.
HIV-1; envelope protein; gpl20; MN-rgpl20; vaccine; AIDS; ss.
HIV-1; envelope protein; gpl20; MN-rgpl20; vaccine; AIDS; ss.
Key
Location/Qualifiers
CDS
                                                                                                                                                                                                                                                                                                                                             DB 1; Length 1501; 25;
                                                                                                                                                                                                                                                       362 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1512;
were obtained from proviral DNA using PCR (see V00533-38).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                    320 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Pred. No. 25;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                    244 C;
                                                                                                                                                                                                                                                                                                                                                1.2%; Score 17; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.2%; Score 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 V00521 standard; DNA; 1512 BP.
                                                                                                                                                                                                                                                575 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          780 atataggaccagggagt 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   780 atataggaccagggagt 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      821 ATATAGGACCAGGGAGT 837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           821 ATATAGGACCAGGGAGT 837
                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 1.2
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-676737.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag=
```

```
completed: September
He: 2194 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search com
Job time:
        888888
                                                                                                                                                                                                           g
                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                          New isolated Enterococcus faecalis polynucleotides - used to develop products for the detection of Enterococcus and for use in vaccines products for the detection of Enterococcus and for use in vaccines of products for prevention or attenuation of Enterococcus infection (laim 1; Page 219; 301pp; English.

The present sequence encodes an antigenic polypeptide fragment asolated from Enterococcus faecalis. The present invention describes genes, proteins and antigenic polypeptides isolated from E. faecalis. The proteins can be used in vaccines for preventing or attenuating an infection caused by a member of the Enterococcus genus in an animal. They can also be used for detecting Enterococcus antibodies in a sample. The nucleotide sequences can be used for detecting Enterococcus nucleic acids. Products from the present invention can also be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                       compounds to identify agonists and antagonists of E. faecalis
      20-APR-1999 (first entry)
Enterococcus faecalis EF121 gene fragment.
Enterococcus faecalis; infection; vaccine; immune response; diagnosis; detection; attenuation; antigenic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated Bornelia burgdorferi nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of infections, particularly Lyme disease (laim 1, Page 1040-1041; 1128pp; English.

X20248 to X20402 represent polynucleotide sequences isolated from Borrelia burgdorferi (Bb). Products derived from Bb can be used for the detection, diagnosis, characterisation, prevention and therapy of Bb infections, e.g. Lyme disease. They can also be used for the production of biosynthetic products, e.g. enzymes. Borrelia belongs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Borrelia burgdorferi polynucleotide sequence #59.

Borrelia burgdorferi; spirochete; bacterium; pathogen; Lyme disease; epidemic relapsing fever; endemic relapsing fever; infection; diagnosis; characterisation; detection; ds.

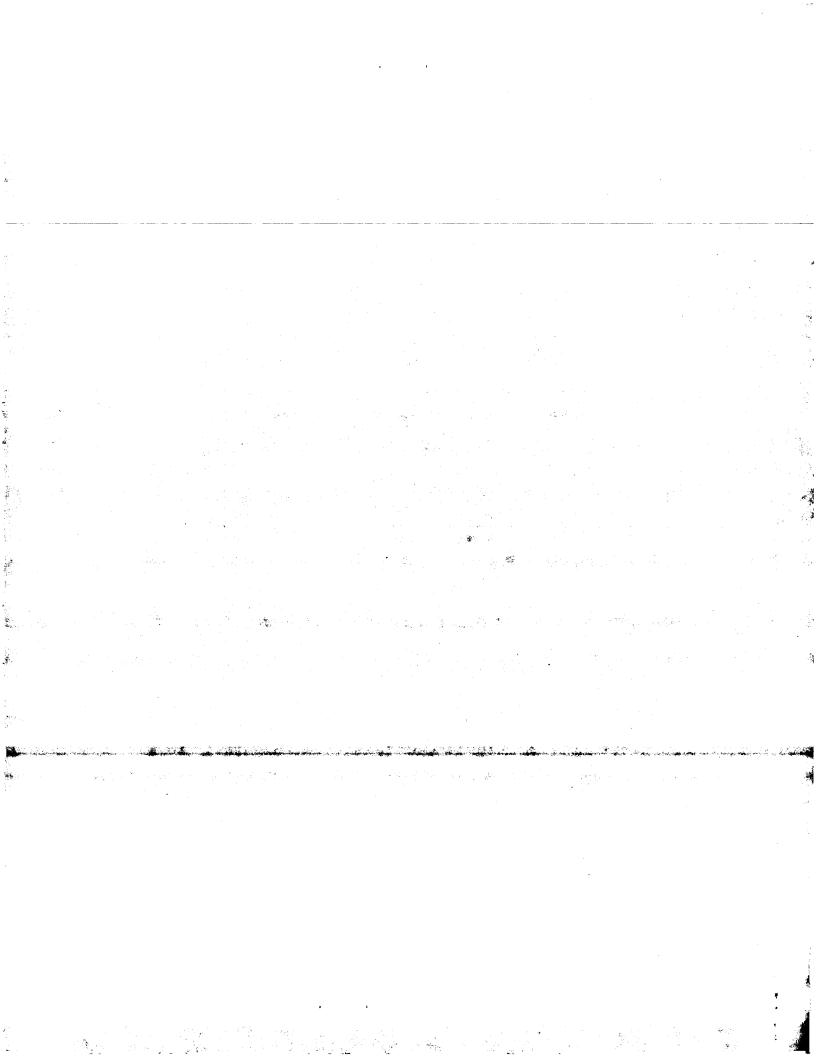
Borrelia burgdorferi.

W09858943-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.2%; Score 17; DB 1; Length 1883; 100.0%; Pred. No. 25; ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R, Dougherty BA, Fraser C, Lathigra R, Smith HO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       404 G;
                                                                                                         12-NOV-1998.
04-MAY-1998; U08959.
14-NOV-1997; US-066009.
16-MAY-1997; US-044031.
16-MAY-1997; US-046655.
(HUMAN GENONE SCI INC.
Bailey C, Choi GH, Hromockyj A, Kunsch CA;
WPI; 99-070095/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       357 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.2.;
100.08; Pr.
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X20306 standard; DNA; 2019 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      666 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1005 CAGTTGCTAAAAATGCC 1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              416 cagttgctaaaaatgcc 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-JUN-1998; U12764.
03-SEP-1997; US-057483.
20-JUN-1997; US-050359,
22-JUL-1997; US-053344.
22-JUL-1997; US-053377.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MEDI-) MEDIMMUNE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 99-081217/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein activity
                                                                                                                                                                                                                  WPI; 99-070095,
P-PSDB; Y00235
                                                                                           WO9850554-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        White OR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clayton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X20306
ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents the Poplar (Populus trichocarpa)

orafleoyl-Coh-O-methyltransferase (CCOAOMT) promoter, PtCCOAOMTI, of the invention. The promoter is specific for plant or tree living vessel elements and/or xylem adjacent ray cells. The promoter is used in genetic modification to provide transgenic plants having altered lighin level and/or composition, which improves digestibility of forages and pulping properties of trees.
to a family of motile, spiral-shaped bacteria called Spirochetes. Spirochetes are pathogenic in humans and Borrelia causes epidemic and endemic relapsing fever, and Lyme borreliosis, more commonly known as
                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                CCOAONT promoter, PtCCOAONT1.
CCOAONT promoter; PtCCOAONT1.
CCOAONT promoter; Poplar; caffeoyl-CoA-O-methyltransferase promoter;
PtCCOAONT1; plant specific promoter; xylem ray cell;
lignin level alteration; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-JUL-1998; E04988.
13-AUG-1997; EP-202507.
(VLAA-) VLAAMS INTERNNIVERSITAIR INST BIOTECHNOG.
BOCTIAN W, Chen C, Meyermans H, Van Montagu M;
WPI; 99-1901697.16.
Poplar caffeoyl-COA-O-methyltransferase (CCOAOMT) promoter -
provide transgenic plants having altered lignin level and/or
                                                                                            798 T;
                                                                                                                                                            DB 1; Length 2019; 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 17; DB 1; Length 3800;
Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1206
                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 701 G;
                                                                                            298 G;
                                                                                                                                                   1.2%; Scole ...
100.0%; Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 26;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               668 C;
                                                                                            312 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.2°,
100.0%; Pt.
                                                                                                                                                                                                                                                                                                                                              RESULT 15
X28141/c
ID X28141 standard; DNA; 3800 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 1b; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1225 A;
                                                                                            611 A;
                                                                                                                                                                                                                                                                                   1906 TGATGATCTTTTAATGC 1922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1111111111111111
2765 ATTTGATCAAGAACTGG 2749
                                                                                                                                                                                                                                           128 tgatgatcttttaatgc 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 100.C
                                                                                                                                                       Ouery Match 1.2
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                924 atttgatcaagaactgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Populus trichocarpa.
W09909188-A2.
                                                                                     2019 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3800 BP;
                                                                      Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-FEB-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 composition
                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
```

9, 2000, 22:03:12



Appli Appli , Appl Appli Appli

Appl Appli Appli Appli Appli

```
Sequence 2
Sequence 2
Sequence 3
                                                                                                                                      Sequence 1
Sequence 1
Sequence 7
                                                                                                                                                                                      Sequence 1
Sequence 7
Sequence 7
Sequence 1
                                                                                  Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                          Sequence
Sequence
Sequence
                                                                   Sequence
                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 26;
11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: KNOL, Jan
APPLICANT: MARCISET, Olivier
APPLICANT: MOLLET, Beat
TITLE OF INVENTION: food-grade microorganisms
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSED: VOGT & O'DONNELL - STEPHEN M. HARACZ
STREET: 707 Westchester Avenue
CITY: WHITE PLAINS
STATE: NY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OFTWARIA STSTEM: C-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/039,866
FILING DATE: 30-MR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92105973
FILING DATE: 07-APR-1992
ATTORNEY AGENT INFORMATION:
NAME: HARACZ, STEPHEN M.
REGISTRATION NUMBER: 33397
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 328-0065
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                    US-08-417-210A-78
US-08-832-883-1
                                                                                                                                                                                                    US-08-832-877-1
US-08-816-1558-7
US-08-716-351A-1
US-08-920-812-6
US-08-920-827-6
                                                                                                                US-08-592-126-85
US-08-106-493A-1
US-08-429-264-1
                                                                                                     PCT-US95-07178-3
                                                                   US-08-475-391-3
US-08-709-609-3
                                                                                                                                                                                                                                                                                          JS-08-921-177-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 1.2%; Score 17; DB Best Local Similarity 100.0%; Pred. No. 11; Matches 17; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08039865
Patent No. 5491079
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-039-866-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
2193
2552
2552
2571
2571
2571
2571
2571
2573
3249
3249
                                                                                                                                                                                      4853
4853
7797
8535
8654
8654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 10604
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-039-866-2/c
                                                                                                              ; Search time 51.17 Seconds
(without alignments)
3876.402 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 38, Appl
Sequence 122, Appl
Sequence 122, Appl
Sequence 32, Appl
Sequence 32, Appl
Sequence 3, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 15, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Appli
Sequence 3, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                      1 cccgggaactccatgtggcc.....aatgcaattcatttggatcc 1442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence Sequence Sequence Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cgn2_6/ptodata/2/ina/5A_COMB.seg:*
/cgn2_6/ptodata/2/ina/5B_COMB.seg:*
/cgn2_6/ptodata/2/ina/5C_COMB.seg:*
/cgn2_6/ptodata/2/ina/5D_COMB.seg:*
/cgn2_6/ptodata/2/ina/6_COMB.seg:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seg:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seg:*
              4.5
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-039-866-3
US-08-541-157A-38
US-08-541-210A-145
US-08-417-210A-145
US-08-65-435A-1
US-08-65-435A-3
US-08-65-435A-3
US-08-65-435A-3
US-08-65-435A-3
US-08-65-435A-3
US-08-843-309-3
US-08-843-309-3
US-08-97-816A-15
US-08-97-816A-17
US-08-530-146-27
US-08-530-146-27
US-08-17-210A-135
US-08-417-210A-135
US-08-417-210A-131
US-08-417-210A-131
US-08-66-61-1
                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-605-501-11
US-07-731-157A-1
US-08-541-780-1
                                                                                                                                                                                                                                                                                                       243080 seqs, 68777915 residues
                                                                                                                9, 2000, 21:11:03
              GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Listing first 45 summaries
                                                                                  - nucleic search, using sw model
                                                                                                                                                                                                                                                      OLIGO_NUC
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Issued_Patents_NA:*
                                                                                                                                                                                    US-09-214-679-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                                                                                                                                                                           seq length: 0
seq length: 1000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2060
                                                                                                                    September
                                                                                                                                                                                                 Perfect score:
Sequence:
                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
                                                                                                                                                                                                                                                                                                                                        Word size :
                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB
Maximum DB
                                                                                OM nucleic
                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database
                                                                                                                  Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               000000
```

ö

Gaps

```
COMPUTER: FLOPPY disk
COMPUTER: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/731,157A
FILING DATE: 19910509
CLASSIFICATION: 435
PRICA PAPLICATION BATA:
APPLICATION NUMBER: EP 90200962
FILING DATE: 18-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER PH.D., BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: 32,750
TELECHOUNICATION INFORMATION:
TELECHOUNICATION INFORMATION:
TELECHOUNE: 415-494-7622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.1%; Score 16; DB 1; Length 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 38, Application US/08541780
Patent No. 5935831
GENERAL INFORMATION:
APPLICANT: Quax, Wilhelmus J.
APPLICANT: Van der Laan, Jan M.
APPLICANT: Lenting, Herman B.M.
ITILE OF INVENTION: Mutated beta-lactam acylase genes
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM STREET: FIVE PALO ALTO SQUARE, 4TH FLOOR
ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM STREET: FIVE PALO ALTO SQUARE, 4TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 1.1%; Score 10, 22
Best Local Similarity 100.0%; Pred. No. 41;
Matches 16; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/541,780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (synthetic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 415-857-0663
TELEX: 380816 COOLEY PA
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   838 tattggtgatgcccat 853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33 TATTGGTGATGCCCAT 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1: 75 base pairs
NUCLEIC ACID
NEDNESS: single
                                                                                                                                                                       ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 435
                               STATE: CALIFORNIA COUNTRY: 1103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-07-731-157A-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 4
US-08-541-780-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGIH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.2%; Score 17; DB 1; Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 38, Application US/0731157A
Patent No. 5457032
GENERAL INFORMATION:
APPLICANT: Quax, Wilhelmus J.
APPLICANT: Wasset, Onno
APPLICANT: Van der Laan, Jan M.
APPLICANT: Lenting, Herman B.M.
TITLE OF INVENTION: Mutated beta-lactam acylase genes NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: KNOL, Jan
APPLICANT: MARCISET, Olivier
APPLICANT: MACLET, Beat
TITLE OF INVENTION: Integrative gene-expression in
TITLE OF INVENTION: food-grade microorganisms
NUMBER OF SEQUENCES: 6
CORRESPONDED.E ADDRESS:
ADDRESSEE: VOGT & O'DONNELL - STEPHEN M. HARACZ
STREET: 707 Westchester Avenue
CITY: WHITE PLAINS
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/039,866
FILING DATE: 30-MAR-1993
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: EP 92105973
FILING DATE: 70-APR-1992
APPCINETYAGENT INFORMATION:
NAME: TARRANGE TO A PARCE OF THE PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 10604
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                        ; Sequence 3, Application US/08039866
; Patent No. 5491079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 1.2%; Scc
Best Local Similarity 100.0%; Pi
Matches 17; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: HARACZ, STEPHEN M.
REGIZETRATION NUMBER: 33397
PELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 328-0055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: DNA (genomic)
US-08-039-866-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (914) 328-0055
TELEFAX: (914) 328-0060
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185 ggagaataacatatgaa 201
                                                185 ggagaataacatatgaa 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 GGAGAATAACATATGAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                   23 GGAGAATAACATATGAA 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
US-07-731-157A-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                 RESULT 2
US-08-039-866-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                δŏ
                                                                                                               qq
```

ö

Gaps

```
RESULT 6
US-08-417-210A-145
Sequence 145, Application US/08417210A
Fatent No. 5863542
GENERAL INFORMATION:
APPLICANT: PADCETTI, ENZO
APPLICANT: TARTAGLIA, JAMES
APPLICANT: TARTAGLIA, JAMES
APPLICANT: TOX, WILLIAM I.
TITLE OF INVENTION: IMMUNOBEFICIENCY RECOMBINANT POXVIRUS
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C.
STREET: 530 FIFTH AVENUE
CITY: NEW YORK
COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PADRES:
COMPUTER: PADRES:
COMPUTER: PADRES:
COMPUTER: PADRES:
COMPUTER: PADRES:
COMPUTER: PATENTING SYSTEM: PC-DOS/MS-DOS.
CURPENUM XNET.
CURPENUM XNET.
CURPENUM XNET.
CURPENUM XNET.
CURPENUM XNET.
CURPENUM XNET.
                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 32, Application US/08967101
Patent No. 5840540
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL ST. GEORGE-HYSLOP, PETER H
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: PRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
                                         Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3; Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,210A
FILING DATE: OS-APR-1995
CLASSIFICATION: 435
                                       DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 05-APR-1995
CLASSIFICATION: 435
ATTONREV/AGENT INPORMATION:
NAME: KOWALSKI, THOMAS J.
REGISTRATION NUMBER: 32,147
REFERENCE/DOCKET NUMBER: 444310-2690
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
                                     Query Match 1.1%; Score 16; DB Best Local Similarity 100.0%; Pred. No. 42; Matches 16; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.1%; Score 16; DB 100.0%; Pred. No. 42; iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 1.1
Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       780 atataggaccagggag 795
                                                                                                                     780 atataggaccagggag 795
                                                                                                                                                53 ATATAGGACCAGGGAG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53 ATATAGGACCAGGGAG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-417-210A-145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-967-101-32
                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: PAOLETTI, ENZO
APPLICANT: TARTAGLIA, JAMES
APPLICANT: COX, WILLIAM I.
TILLE OF INVENTION: IMMUNOBERICIENCY RECOMBINANT POXVIRUS
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING JATE: MEBER: EP 90200962
FILING DATE: 18-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER PH.D., BARBARA
REGISTRATION NUMBER: 32,750
REPERBENE_COCKET UNDRER: GRO-027/00US
TELEPRATION INFORMATION:
TELEPAN: 415-897-0663
TELEFAX: 380816 COOLEY PA
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 75 base pairs
TYPE: nucleic acid
STRANDEDINESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C. STREET: 530 FIFTH AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 1.1%; Score 16; DB Best Local Similarity 100.0%; Pred. No. 41; Matches 16; Conservative 0; Mismatches
             APPLICATION NUMBER: US/07/731,157 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 122, Application US/08417210A Patent No. 5863542 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: DNA (synthetic): HYPOTHETICAL: NO US-08-541-780-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     838 tattggtgatgcccat 853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33 TATTGGTGATGCCCAT 48
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: NEW YORK STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-417-210A-122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-417-210A-122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
```

ö

```
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Skatrud, Paul
APPLICANT: Peery, Robert
APPLICANT: Hoskins, Joann
APPLICANT: Wu, Chyun-Yeh Earnest
TITLE OF INVENTION: Biosynthetic Gene MurD of Streptococcus
TITLE OF INVENTION: pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 1350; 45;
                                                                                                                                                                                                                        Length 475;
                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
SUFTRANCY APPLICATION DATA:
APPLICATION NUMBER: US/08/665,435A
                                                                                                                                                                                                                         Score 16; DB 4; Pred. No. 44; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Eli Lilly and Compa
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08665435A Patent No. 5681694 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Webster, Thomas D
REGISTRATION NUMBER: 39,872
REFERENCE/DOCKET NUMBER: X-99
TELECHOWNICATION INFORMATION:
TELEPHONE: 317-276-3334
TELEPHONE: 317-276-3861
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEO ID NO: 32:
SQUENCE CHARACTERISTICS:
LENGTH: 475 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 1350 base pairs TYPE: nucleic acid sTRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: DNA(genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                  972 aaaatattatgagtat 987
                                                                                                                                                                                                                               Query Match 1.1
Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                     37 AAAATATTATGAGTAT 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY:
; LOCATION:
US-08-665-435A-1
                                                                                                                                                                                                                                                                                                                                                                                                             US-08-665-435A-1
                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 32, Application US/08592541
| Sequence 32, Application US/08592541
| Patent No. 5986054
| GENERAL INFORMATION:
| APPLICANT: ROWAENS, JOHANNA M
| APPLICANT: ROWAENS, JOHANNA M
| APPLICANT: ROWAENS, PAUL E
| TILLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
| TILLE OF INVENTION: TO ALZHEIMER'S DISEASE
| NUMBER OF SEQUENCES: 183
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: High Street Tower - 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                     PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
1.1%; Score 16; DB 3;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 16; Conservative 0; Mismatches (
                     CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: DNA (genomic) US-08-967-101-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 475 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  972 aaaatattatgagtat 987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37 AAAATATTATGAGTAT 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 800
                                                                                               Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                 STATE: Massachus
                                               ADDARST: nr.
STREET: nr.
Trw: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                  ZIP: 02110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-592-541-32
```

à

```
APPLICANT: Statrud, Paul
APPLICANT: Peery, Robert
APPLICANT: Hoskins, Joann
APPLICANT: Wu, Chyun-Yeh Earnest
TITLE OF INVENTION: Biosynthetic Gene Mur D of Streptococcus pneumoniae
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3; Length 1350; 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPTTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/843,309
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Webster, Thomas D
REGISTRATION NUMBER: 39,872
REFERENCE/DOCKET NUMBER: X 9900
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAM: 317-276-3334
TELEFRAM: 317-276-33861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 16;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/843,309
                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08843309
Patent No. 5834270
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.1%;
illarity 81.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1350 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1117 gctgggcaacatggtc 1132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              409 GCUGGGCAACAUGGUC 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: mRNA HYPOTHETICAL: NO
  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-843-309-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-843-309-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Skatrud, Paul
APPLICANT: Peerry, Robert
APPLICANT: Hoskins, Johan
APPLICANT: Wu, Chyun-Yeh Earnest
TITLE OF INVENTION: Biosynthetic Gene Mur D of Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
  ö
                                                                                                                                                                                                                                                 APPLICANT: Skatrud, Paul
APPLICANT: Skatrud, Paul
APPLICANT: Peery, Robert
APPLICANT: Hoskins, Joann
APPLICANT: Wu, Chyun-Yeh Earnest
TITLE OF INVENTION: Biosynthetic Gene Murb of Streptococcus
TITLE OF INVENTION: pneumoniae
WUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 16; DB 1; Length 1350;
Pred. No. 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWAR APPLICATION DATA:
APPLICATION NUMBER: US/08/665,435A
  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Ell Lilly and Company STREET: Lilly Corporate Center CITY: Indianapolis STATE: COUNTRY: US
                                                                                                                                                                                       Sequence 3, Application US/08665435A Patent No. 5681694 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Webster, Thomas D
REGISTRATION UNDRER: 39,872
REFERENCE/DOCKET NUMBER: x-99(
TELECOMMUNICATION INFORMATION:
TELEFAX: 317-276-334
TELEFAX: 317-276-3861
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 1350 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08843309
Patent No. 5834270
  .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                          1117 gctgggcaacatggtc 1132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     409 GCUGGGCAACAUGGUC 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 1.1
Best Local Similarity 81.2
Matches 13; Conservative
                                                                                 409 GCTGGGCAACATGGTC 424
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ANTI-SENSE:
US-08-665-435A-3
                                                                                                                                                                     US-08-665-435A-3
16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-843-309-3
  Matches
```

g

ö

Gaps

```
Sequence 27, Application US/08037816A
Patent No. 586524
GENERAL INFORMATION:
APPLICANT: Hasel, Karl W.
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: THERETO, AND THERAPEUTIC AND PROPHYLACTIC USES TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1532;
                                                                                               Length 1532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: New York
COUNTRY: USA
ZIP: New YORK
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PROPER PROPER PROPER PROPERTION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/037,816A
FILING DATE: 26-MAR-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
RAME: White, John P. RECISTRATION UNBER: 28,678
REFERENCE/DOCKET NUMBER: 41190/JFW/AJM
TELEFRAY: (212) 664-6525
TELEFRAX: (212) 664-6525
TELEFRAX: (212) 664-6525
TELEFRAX: (212) 664-6525
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.1%; Score 16; DB
100.0%; Pred. No. 46;
ive 0; Mismatches
                                                                                                     Score 16; DB 3
Pred. No. 46;
0; Mismatches
                                                                                         1.1%; SCC-
100.0%; Pre
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1532 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   780 atataggaccagggag 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 16; Conservative
                                                                                                       Query Match
Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                    780 atataggaccagggag 795
                                                                                                                                                                                                                          932 ATATAGGACCAGGGAG 947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION:
US-08-037-816A-27
        CCATION: 1.1522
COTHER INFORMATION:
US-08-037-816A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: li
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                      RESULT 14
US-08-037-816A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                            qq
                                                                                                                                                                                          δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15, Application US/08037816A
Patent No. 5869624
GENERAL INFORMATION:
APPLICANT: Hasel, Karl W.
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: THEREFO AND THERAPEUTIC AND PROPHYLACTIC USES
TITLE OF INVENTION: THEREFO NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                Length 1353;
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
1.1%; Score 16; DB 3;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 16; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC COMPAILS
COMPUTER: PATCHIN FELESCHIL SOFTH
COMPARED: PATCHIN FORMATION SOFTH
APPLICATION NUMBER: US/08/037,816A
FILING DATE: 26-MAR.1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P. REGISTRATION NUMBER: 41190/JPW/AJM
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SOFTH
TELEFONGE: (212) 977-9550
TELEFA: (222) 664-0525
TELEFA: (222) 664-0525
INFORMATION FOR SEG ID NO: 15:
SEGURENCE CHARRACTERISTICS:
LINDRANCE: MACHERICATERISTICS:
LEGGTH: 1532 base pairs
NAME: Webster, Thomas D
REGISTRATION NUMBER: 39,872
REFERENCE/DOCKET NUMBER: X-9900
TELECOMMUNICATION INFORMATION:
TELEPRAN: 317-276-3841
INFOREMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1353 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Cooper & Dunham STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: DNA(genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1117 gctgggcaacatggtc 1132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      409 GCTGGGCAACATGGTC 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                          1..1353
                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
                                                                                                                                                                                                                                                                                ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
US-08-037-816A-15
                                                                                                                                                                                                                                                                                                                                          ;
US-08-843-309-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ολ
```

ö

Gaps

```
Sequence 15, Application US/08530146

| Sequence 15, Application US/08530146
| Patent No. 5886163
| Sequence 15, Application US/08530146
| Patent No. 5886163
| GENERAL INFORMATION:
| APPLICANT: Hasel, Karl W. APPLICANT: AND THEREOF AND THEREOF AND THEREOF AND THEREOF AND PROPHYLACTIC USES TITLE OF INVENTION: THEREOF AND THEREOF ADDRESS:
| ADDRESSEE: Cooper & Dunham STREET: 30 ROCKEfeller Plaza CITY: New York STATE: New York STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTY: USA

ZIP: 10112

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/530,146

FILING DATE:

CLASSIFICATION DATA:

APPLICATION NUMBER: US/08/037,816

FILING DATE: 26-MAR-1993

ATTORNEY AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET UNMBER: 41190/JPW/AJM

TELECOMMUNICATION INFORMATION:

TELEFAX: (212) 977-9550

TELEFAX: (212) 977-9550

TELEFAX: (212) 977-9550

TELEFAX: (212) 664-0525

TELEFAX: (212) 664-0525

TELESAX: (212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS

LOCATION: 1..1522

CTHER INFORMATION:

US-08-530-146-15
RESULT 15
US-08-530-146-15
```

```
Gaps
                                                  ó
Query Match
1.1%; Score 16; DB 3; Length 1532;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                ò
```

<sup>780</sup> atataggaccagggag 795

셤

Search completed: September 9, 2000, 22:01:48 Job time: 3045 sec

• \*

```
gb_gss10:*
gb_gss11:*
em_gss12:*
gb_gss12:*
                                                                                                                                                                                                                                                                                                                                                                                                            9b_9ss5:*
9b_9ss6:*
9b_9ss7:*
9b_9ss8:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    em_gss10:*
      em_gss5:*
em_gss6:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           em_gssll:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     em_gss8:*
September 9, 2000, 20:45:57 ; Search time 585.75 Seconds
(without alignments)
10856.120 Million cell updates/sec
                                                                          US-09-214-679-1
1442
1 cccgggaactccatgtggcc.....aatgcaattcatttggatcc 1442
                                                                                                                                                        10495684
     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                           5247842 seqs, 2204914090 residues
                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                          Post-processing: Listing first 45 summaries
                                  OM nucleic - nucleic search, using sw model
                                                                                                        OLIGO_NUC
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                             1: em_est1:*
2: em_est2:*
4: em_est3:*
6: em_est5:*
6: em_est5:*
6: em_est6:*
6: em_est1:*
                                                                                                                                                                                                                                                                                                                                                           gb_est2::
gb_est4::*
gb_est6::*
gb_est6::*
gb_est7::*
gb_est9::*
gb_est10::*
                                                                                                                                                                                                                                                                                                                                                                                                                                 gb_est12:*
gb_est13:*
gb_est14:*
gb_est15:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                             gb_est16:*
gb_est17:*
gb_est18:*
gb_est18:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gb_est23:*
gb_est24:*
                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 1000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gb_est20:
gb_est21:
gb_est22:
                                                                                                                                                                                                          EST:*
                                                                                   Perfect score:
                                                                                                       Scoring table:
                                                                                                                                         Word size :
                                                                                                                                                                                                          Database :
                                                                                           Sednence:
                                                                                                                            Searched:
                                                Run on:
```

```
gb_gss15:*
gb_gss16:*
gb_gss17:*
gb_gss18:*
gb_gss13:*
gb_gss14:*
                                              gb_gss19:*
                                                     em_gss13:*
1117:
1118:
1119:
120:
121:
122:
123:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

( pases 1 to 409)

Mahairas, G.G., Zackrone, K.D., Smith, T., Tipton, S., Schmidt, S., Traicoff, R., Abajian, C., Blanchard, A., West, A. and Hood, L.E. Construction of a Characterized Clone Resource for Genomic Sequencing: Generation and Preliminary Analysis of 20,000 Sequence

B44876.1 GI:2549710

Homo sapiens

ORGANISM

KEYWORDS

VERSION SOURCE REFERENCE

AUTHORS

TITLE

human.

survey sequence. B44876

ACCESSION

Tagged Connectors
Unpublished (1997)
On Dec 15, 1999 this sequence version replaced gi:4213071.
Contact: Mahaington
Seattle, Wa 98195, USA
Tel: (206) 616-8744
Fax: (206) 685-7301
Sequence Tagged Connector
Plate: CT 782, row: M column: 11

JOURNAL COMMENT

Description		876 F	W66727 me26d06.rl	57770 41461	56799 39389	26093 18169	357182 4006	za53c02.s	65b11.s	65 AU0068	126 RPCI-1	C79644 Mo	55 HS 5300	3 UI-R-BT	0 AV19	C68576 Yu	6 AV2037	M89105 CEL16D1 Chr	AA799513 EST189010	AI555490 UI-R-C2p-	B36341 HS-1039-A1-	H76674 17105 Lambd	AQ036697 CIT-HSP-2	AI995150 701502362	AW435445 UI-R-BJ0p	9 tw49a08.	Η	20 HS_317	8 xb58c10.	5 CIT-HSP-	34626	C37085 Yuj	.5 UI-R-YO-	1 ts96f1	15144 C15144 C	2966 C82966 r	3822 C8	07 D86807	993 gb23	yr74b09.	51 <u>2</u> aa95	44901 UI-R-B	35528 ra21c1	35654 ra25h09.	552960 ns71d0	853 HS_2185_
QI.		44	1 W66727	1 AW35777	1 AW35679	1 AW32	1 AW35718	7 N74	1 w87	7 AU00686	03 AQ	1 C79	04 AQ5972	5 AI146	1 AV19360	1 C68	1 AV203	6 M8910	1 AA7995	1 AI55549	20 B3634	Н 9	3 AQ03669	7 AI99515	2 AW43544	2 AI683139	19 AZ0371	14 AQ80372	3 AW08197	3 AQ07943	0 C34626	0 C37085	5 AI112	6 AI91729	0	1 C8296	1 C8382	1 D86807	ν 9	6 H65770	7 AA48751	5 AI1449	0 AW73552	0 AW73565	9 AA652	3 AQ0228
Length DB		409 1	S	40	4	-	19	59	8	2	20	72	95	30	9	94	78	29 8	40 3	56 4	84 1	8 60	10 9	27 4	57 7	563 4	92 1	36 1	43 6	27 9	8 00	8 00	01 3	11 4	39 8	87 8	8 2	91 8	8 96	03 8	10 2	14 3	22 8	20		
% Query Match		1.5		1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	٠	٠	٠	٠			٠	•		٠			1.3	٠	٠	•		•	•	٠		٠	٠	٠									1.2
Score	1	21	21	20	20	20	20	20	20	20	20	20	20	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	19	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	81,	ят
ult No.		-	7	m	4	N.	9	7	ω	Φ	10	11	12	13	14	15	16	11	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	32	36	37	38	36	40	41	42	43	44	45
Result No.	1	υ	O												Ö						υ	ပ		ပ				O		υ						O			υ							U

ö

Gaps

ö

1.5%; Score 21; DB 120; Length 409; 100.0%; Pred. No. 0.85; cive 0; Mismatches 0; Indels

Query Match 1.5 Best Local Similarity 100. Matches 21; Conservative

ţ

/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones E-Co11 DH10B"

127 t

90 9

82 C

๙ 110

BASE COUNT ORIGIN

/organism="Homo sapiens" /db\_xref="taxon:9606" /clone="Plate=CT 782 Col=11 Row=M" /clone\_lib="CIT Human Genomic Sperm Library C" /sex="M"

High quality sequence stop: 409. Location/Qualifiers

source

FEATURES

Class: BAC ends

```
י מס
                     ALIGNMENTS
```

B44876 409 bp DNA GSS 21-OCT-1997 HS-1060-A1-G06-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 782 Col=11 Row=M, genomic

DEFINITION RESULT 1 B44876/c LOCUS

•}

```
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (Dases 1 to 454)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                             W66727 454 bp mRNA EST 14-JUN-1996
me26d06.rl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The Washu-Himi Mouse EST Project
Unpublished (1996)
On Jan 7, 1998 this sequence version replaced gi:636815.
Contact: Marra M.Mouse EST Project
Washu-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                              clone IMAGE:388619 5', mRNA sequence.
                      197 atgaaatggttggaagaatcc 217
                                                                                                                                                                                                                                                          W66727.1 GI:1375662
                                                                                                                                                                                                                                                                                                         house mouse.
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Waterston, R.
                                                                                                                                                                                        DEFINITION
                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
JOURNAL
COMMENT
                                                                                                                 RESULT 2
W66727/c
LOCUS
                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                        VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                         d
  δŏ
```

```
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus
                                                                                                                                                                                                                                                                                                                                                  33 a
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                             Source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
                                                                                                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
AW356799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Design and use of four pooled tissue normalized CDNA libraries for EST discovery in cattle Unpublished (2000)
Unpublished (2000)
Un Jan 6, 2000 this sequence version replaced gi:6676822.
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center,
USDA, ARS, US Weat Animal Research Center,
USDA, ARS, 162, 4366
Fax: 402 762 4366
Fax: 402 762 4360
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred single pass sequencing. Bases called by cross_match with the -minscore 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T 3'), on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos (total RNA provided by Minoru Ko, Wayne
State Univ., from 2 ]; double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT/T3 vector. Library went through one round of
normalization, and was constructed by Bento Soares and
                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovidae; Bovidae; Bos.

1 (bases 1 to 240)
Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A. and
                                                                     This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:240451
Seq primer: ETPrimer
High quality sequence stop: 341.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-FEB-2000
                                                                                                                                                                                                                   /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:388619"
/clone_1lb="Soares mouse embryo NbMEl3.5 14.5"
/sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.5%; Score 21; DB 91; Length 454;
100.0%; Pred. No. 0.85;
ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AW357770 240 bp mRNA EST
41461 MARC 3BOV Bos taurus CDNA 5', mRNA sequence.
AW357770
                                                                                                                                                                                                                                                                                                                                              /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134 t
                                                       Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M.Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     904 aatcaccaccatcaaagtcga 924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49 AATCACCACCATCAAAGTCGA 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AW357770.1 GI:6861776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                   Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                    1. .454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ಡ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66
                                                                                                                                                                                                      Source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
AW357770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCUS
```

ò g

```
Unpullished (2000)
Unpullished (2000)
Un Jan 6, 2000 this sequence version replaced gi:6675823.
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4366
Fax: 402 762 4360
Fax: 402 762 4360
Fax: 402 762 4360
Fax: 402 762 4360
Fax: Vector identified and trimmed with phred
V0.980904.e. Vector identified by cross_match with the -minscore 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                          /organism="Bos taurus"
/db_xref="taxon:9913"
/db_xref="taxon:9913"
/tclone_lib="WARC 3BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCWV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendonosus muscle, and fetal longissimus muscle."
75 c 59 g 73 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Design and use of four pooled tissue normalized cDNA libraries for EST discovery in cattle Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bosiae; Bos.
1 (bases 1 to 245)
Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="pooled"
/lab_nost="DHIDB"
/note="Vector: pGMV SPORT6; Site_1: Xbal; Site_2: Xhol;
Library made from pooled tissue from marrow, alveolar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.4%; Score 20; DB 71; Length 240; 100.0%; Pred. No. 3.1; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AW356799 245 bp mRNA EST
39389 MARC 3BOV Bos taurus CDNA 5', mRNA sequence.
AW356799
PCR PRIMERS
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCCCAGTCACGACG
Plate: 18 row: N column: 4
Seg primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and inimatch 12 options.
PCR PRimers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTTCCAGTCACGAC
Plate: 15 row: H column: 16
Seq primer: ATTTAGGTGACATAGG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9913"
/clone_lib="MARC 3BOV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       420 tgctaaaaatgccctttctc 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AW356799.1 GI:6860805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 TGCTAAAATGCCCTTTCTC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 20; Conservative
```

03-FEB-2000

```
Bos taurus.
Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N74414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST.
                                                                         KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
AW357182
LOCUS
DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
SOURCE
                                                                                                                                                                        REFERENCE
                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                   TITLE
                                                                                                                                                                                                                                                                               COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N74414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
Single pass sequencing. Bases called and trimmed with the -minscore 20
and -minmatch 12 options.
POR PRIMER:
PORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 5 row: I column: 23
Seq primer: ATTTAGGTGACATARGG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Design and use of four pooled tissue normalized cDNA libraries for EST discovery in cattle Unpublished (2000) On Jan 6, 2000 this sequence version replaced gi:6675590. Contact: Smith TPL USDA, ARS, US Meat Animal Research Center Tel: 402 762 4366 Fex: 402 762 4366
                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinee; Bos.

1 (bases 1 to 261)
Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A. and
macrophage, ovary, fetal semitendonosus muscle, and fetal longissimus muscle. ^{\rm H} 64 t ^{\rm 64} c ^{\rm 47} g ^{\rm 64} t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pCMv sporf6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from lymph node, ovary,
fat, hypothalamus, and pituitary."
7 c 55 g 65 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                             Gaps
                                                                                                                                                                                                                                                                  27-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.4%; Score 20; DB 71; Length 261; llarity 100.0%; Pred. No. 3.1; Conservative 0; Mismatches 0; Indels
                                                                                             Score 20; DB 71; Length 245; Pred. No. 3.1;
                                                                                                                                                                                                                                                      AW326093 261 bp mRNA EST :
18169 MARC 1BOV Bos taurus CDNA 5', mRNA sequence.
AW326093
                                                                                                                             0; Indels
                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 180V"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                   1.4%; Sco
Similarity 100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AW326093.1 GI:6762014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1..261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
20; Conserv
                                                                                                                                                                                                                                                                                                                                                  Bos taurus.
Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Keele, J.W.
                                       ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44
                                       47
                                                                                                  Query Match
Best Local Simi
Matches 20;
                                                                                                                                                                                                                                                                                                                                   EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                       BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                           RESULT
AW326093
                                                                                                                                                                                                                                                                                                                                   KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                                                                                                                                                                      VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                 õ
                                                                                                                                                                                             g
```

RESULT

```
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Exar: 402 762 4360
Exar: 402 762 4300

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N74414 329 bp mRNA EST 19-MAR-1996 za53c02.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:296258 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Buwaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 329)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Hollman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Design and use of four pooled tissue normalized CDNA libraries for EST discovery in cattle Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: Xba1; Site_2: Xho1;
Library made from pooled tissue from testis, thymus,
semitendonosus muscle, longissimus muscle, pancreas,
adrenal, and endometrium."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovo Bovidae; Bovinae; Bos.

1 (bases 1 to 279)
Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 20; Conservative 0; Mismatches 0; Indels
AW357182 279 bp mRNA EST (
40066 MARC 2BOV Bos taurus CDNA 5', mRNA sequence.
AW357182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_llb="MARC 2BOV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCCCAGTCACGACG
Plate: 23 row: I column: 15
Seq primer: ATTTAGGTGACATATAG.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AW357182.1 GI:6861188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N74414.1 GI:1231699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             o 96
```

```
/db_xref="tbo:122255"
/db_xref="tbo:122255"
/clone="IMAGE:416925"
/clone="IMAGE:416925"
/clone="lib="Soares_fetal_liver_spleen_INFLS_SI"
/sex="male"
/dev_stage="20 week-post conception fetus"
/dab_host="blind fampicillin resistator"
/lab_host="blind fampicillin resistator"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
This is a subtracted version of the original soares fetal
liver spleen INFLS library.
Ist strand CDNA was primed
with a Pac I - oligo(dT) primer [5' trand CDNA was primed
with a Pac I - oligo(dT) primer [5' trand cDNA was primed
with a Pac I - oligo(dT) primer [5' trand cDNA was primed
with a Pac I - oligo(dT) primer [5' trand cDNA was primed
with a Pac I - oligo(dT) primer [5' trand cDNA was primed
with a Pac I - oligo(dT) primer [5' trand cDNA was primed
with a Pac I - oligo(dT) primer [5' trand cDNA was primed
with a Pac I - oligo(dT) primer [5' trand cDNA was primed
with a Pac I - oligo(dT) primer [5' trand cDNA was primed
with a Pac I - oligo(dT) primer [5' trand cDNA was primed
with a Pac I - oligo(dT) primer [5' trand cDNA was primed
with a Pac I - oligo(dT) primer [5' trand cDNA was primed
with a Pac I - oligo(dT) primer [5' trand cDNA was primed
with a Pac I - oligo(dT) primer [5' trand cDNA was primed
with a Pac I - oligo(dT) primer [5' trand cDNA was primed
with a Pac I - oligo(dT) primer [5' trand cDNA was primed
with a Pac I - oligo(dT) primer [5' trand cDNA was primed
with a Pac I - oligo(dT) primer [5' trand cDNA was primed
with a Pac I - oligo(dT) primer [5' trand cDNA was primed
with a Pac I - oligo(dT) primer [5' trand cDNA was primed
with a Pac I - oligo(dT) primer [5' trand cDNA was primed
with a Pac I - oligo(dT) primer [5' trand cDNA was primed
with a Pac I - oligo(dT) primer [5' trand cDNA was primed
with a Pac I - oligo(dT) primer [5' trand cDNA was primed
with a Pac I - oligo(dT) primer [5' trand cDNA was primed
with a Pac I - oligo(dT) primer [5' trand cDNA was primed
with a Pac I - oligo(dT) primer [
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="spc01051"
/clone_lib="Schizosaccharomyces pombe late log phase cDNA"
/sex="h minus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to \bar{4}20) Morimyo,M. and Mita,K. Identification of expressed sequence tags of Schizosaccharomyces
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 620 Std Error: 0.00
Seq primer: mob.REGA+ET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AU006865 420 bp mRNA EST 31-JUL-1998
AU006865 Schizosaccharomyces pombe late log phase cDNA
Schizosaccharomyces pombe cDNA clone spc01051, mRNA sequence.
AU006865.1 GI:3343323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome Research Group
National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
Email: morimyo@nis.go.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dipublished (1998)
On May 14, 1999 this sequence version replaced gi:4827815.
Contact: Mitsuoki Morimyo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales;
Schizosaccharomycetaceae; Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: Ml3mpl9; The cDNA library of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 91; Length 382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Schizosaccharomyces pombe"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.4%; Score 20; DB
100.0%; Pred. No. 3.2
iive 0; Mismatches
                                                                                                                                                                                                                               1. 382
/organism="Homo sapiens"
/db_xref="GDB:1325395"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:4896"
                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        386 gctatcaattcggaacagga 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="972"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33 GCTATCAATTCGGAACAGGA 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 1.4°
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fission yeast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pombe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                     source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AU006865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 382)
Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins,M., Hullman,M., Kucaba,T., Lacy,M., Le,M., Le,N., E., Moore,B., Mooris,B., Morris,M., Parsons,J., Prange,C., Rikin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry,Meg,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             382 bp mRNA EST 02-FEB-1997 clone IMAGE:416925 3', mRNA sequence. W87700 GI:1401754 EST.
                                                                                                                                                                                                                                                                                  This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: ml3 -40 forward High quality sequence stop: 308.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                    The Washu-Merck EST Project
Unpublished (1995)
Unpublished (1995)
Con Dec 20, 1995 this sequence version replaced gi:1133302.
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           On Jan 5, 1998 this sequence version replaced gi:1327905.
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                           1. .329
/organism="Homo sapiens"
/db_xref="GDB:1241179"
/db_xref="taxon:9606"
/clone="IMAGE:296258"
/clone_lib="Soares fetal liver spleen lNFLS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 20; DB 87; Length 329;
Pred. No. 3.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0%; P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    386 gctatcaattcggaacagga 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 GCTATCAATTCGGAACAGGA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and Marra, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97044478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
                       TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
W87700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOURCE
```

ö

```
Systematic analyses of genes expressed in 3.5-dpc mouse blastocyst (The ERATO/Doi Project at Wayne State University) Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                       Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 595)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. an
                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 572)
Ko,M.S.H., Kitchen,J.R., Wang,X., Wang,X., Threat,T.A., Sun,T.,
Grahovac,M.J., Mason,S., Lim,M.K., Paonessa,P.D., Sauls,A.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Hirofumi Doi
Doi Bioasymmetry Project, ERATO
Japan Science and Technology Corporation (JST)
WBG Marive East 12F, 2-6 Nakase, Mihama-ku, Chiba 261-71, Japan
Email: hdebioa.jst.go.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSS 08-JUN-1999
Human Male BAC Library Homo sapiens
1-21 Row=B, genomic survey sequence.
                                                                                                                                        C79644 572 bp mRNA EST 26-JUN-1998
C79644 Mouse 3.5-dpc blastocyst cDNA Mus musculus cDNA clone
J0009G09 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence-tagged connectors: A sequence approach to mapping scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.4%; Score 20; DB 81; Length 572;
100.0%; Pred. No. 3.3;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="J0069G09"
/clone="Jib="Mouse 3.5-dpc blastocyst cDNA"
/tissue_type="blastocyst"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AQ597255 595 bp DNA
HS_5300_B1_A11_T7A RPCI-11 Human Male
genomic clone Plate=876 Col=21 Row=B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .572
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="3.5-dpc"
136 c 113 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
936 actggcagctttcctggcca 955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   354 ACTGGCAGCTTTCCTGGCCA 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQ597255.1 GI:5028467
                                                                                                                                                                                                                                                                 C79644.1 GI:2519974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQ597255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hood, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dol, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human.
                                                                                                                                                                                                                                           C79644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                 VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQ597255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMMENT
                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGIN
                                                                                                                                                                                                                                                                                                              SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                 g
    δ
Schizosaccharomyces pombe was prepared by cloning cDNA into the Smal site of Ml3mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, http://www.nirs.go.jp)" 62 c 78 g 124 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@tesgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIll Human Male BAC Library"
8 0 c 109 g 187 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQ529126 550 bp DNA GSS 18-MAY-1999 RPCI-11-368P15.TV RPCI-11 Homo sapiens genomic clone RPCI-11-368P15, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Map Building

Multished (1997)

On Sep 10, 1998 this sequence version replaced gi:355790.

On Sep 10, 1998 this sequence version replaced gi:355790.

Other_GSS: RPCI-11-368P15.TJ

Other_GSS: RPCI-11-368P15.TJ

Contact: Shaying Zhao, William Nierman, Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 550)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and
Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 550;
                                                                                                                                                                                                           Score 20; DB 47; Length 420;
Pred. No. 3.2;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 1.4%; Score 20; DB 103; Best Local Similarity 100.0%; Pred. No. 3.3; Matches 20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1. 550
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="RPCI-11-368P15"
/clone_lib="RPCI-11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="GDB:7641302"
/db_xref="taxon:9606"
                                                                                                                                                                                         1.4%; Scor.
" 100.0%; Pre
                                                                                                                                                                                                                                                                                                                   960 tggagaatgccgaaaatatt 979
                                                                                                                                                                                                                                                                                                                                            331 TGGAGAATGCCGAAAATATT 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQ529126.1 GI:4841239
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="Male"
                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: T7
Class: BAC end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQ529126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human.
                                                                                                                                                                                                                                                                      20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
                                                                                                                         BASE COUNT
                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VĒRSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AQ529126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMMENT
                                                                                                                                               ORIGIN
                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                               g
```

ö

Gaps

ö

نډ 167 and

```
/organism="Caenorhabditis elegans"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Concerning the control of Genetics
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:6239"
/clone="yk619c5"
                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans.
Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1001 ccgctggaggatgcgacgc 1019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AV193600.1 GI:5575752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="N2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                276 CCGCTGGAGGATGCGACGC 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 1.39
Best Local Similarity 100.0
Matches 19; Conservative
                                                                                               POLYA-NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
AV193600/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3867
Fax: (206) 616-3887
Email: jwallacedu washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genefics (info@fresgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 876 row: B column: 21
Seq priner: T7
Class: BAC ends
High quality sequence stop: 595.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   University of Iowa 451 Eckstein Medical Research Building Iowa City, IA 52242, USA 7e1: 319 335 8256
Fax: 319 335 9565
Email: msoares@blue.weeg.ulowa.edu
Oligo-dr track not found, Not I site shown in beginning of sequence is likely internal to the message. CDNA Library Preparation: M. Fatima Bonaldo, Ph.D. Clone distribution: clones will be available through Research Genetics This clone is also available through the
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xxef="taxons agricus"/db_xxef="taxons agricus"/db_xxef="taxons agricus"/clone="plate=876 Col=21 Row=B"
/clone="lb="RPCI-11 Human Male BAC Library"
/sex="male"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
/note="Vector: pBACe3.6; Site_1 = complainty dispersed with a combination of EcoRI and partially dispersed with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AI146143 330 bp mRNA EST 05-JUL-1999 UI-R-BTO-qh-h-04-0-UI.sl UI-R-BTO Rattus norvegicus cDNA clone UI-R-BTO-qh-h-04-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                On Apr 7, 1998 this sequence version replaced gi:3035792.
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.4%; Score 20; DB 104; Length 595; 100.0%; Pred. No. 3.3; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193 t
                                                                                                                                                                                                                                                                                                                                                                                                                     1. .595 // /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Res. 6 (9), 791-806 (1996) 97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1178 gtttagtaggaataactaac 1197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421 GTTTAGTAGGAATAACTAAC 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AI146143.1 GI:3667942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 330)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ၁
96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 1.4
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Norway rat.
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AI146143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 1:
A:146143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
       COMMENT
```

ŏ

```
/Grainsing and the state of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AV193600 360 bp mRNA EST 22-JUL-1999
AV193600 Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite
embryo Caenorhabditis elegans CDNA clone yk619c5 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoo; Nematoda; Chromadorea; Rhabditida;
Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 360)
Kohara,Y., Shin-1,T., Thierry-Mieg,J., Thierry-Mieg,D., Mitsuki,H.,
Nishigaki,A., Motohashi,T., Zeng,Q., Watanabe,H., Sugimoto,A.,
Sano,M., Miyata,A., Mitani,Y., Iida,K., Uesugi,H., Sugimoto,A.,
Nomoto,H.
I.M.A.G.E. Consortium at LLNL (info@image.llnl.gov). IMAGE ID=1/8816 The following repetitive elements were found in this CDNA sequence: 55-85, >GC_rich#Low_complexity seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Expressed genes in C.elegans unpublished (1999) On Jul 9, 1999 this sequence version replaced gi:5434899. Contact: Yuji Kohara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.3%; Score 19; DB 35; Length 330;
100.0%; Pred. No. 12;
Live 0; Mismatches 0; Indels

    .330
    /organism="Rattus norvegicus"
```

```
;
0
                                                                                                                                                                                                      ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genorhabditis elegans.

Caenorhabditis elegans.

Caenorhabditis elegans.

Caenorhabditis elegans.

EST.

Caenorhabditis elegans.

Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

I (bases 1 to 376)

I (bases 1 to 376)

Expression map of the C.elegans genome

Unpublished (1966)

On Jun 15, 1998 this sequence version replaced gi:3224348.

On Jun 15, 1998 this sequence version replaced gi:3224348.

On Jun 15, 1998 this sequence version replaced gi:3224348.

Contact: Yuji Kohara

Gene Library Lab

National Institute of Genetics

Yata 1111, Mishima, Shizuoka 411, Japan

Tel: 81-559-81-6854

Fax: 81-559-81-6855

Email: Ykohara@lab.nig.ac.jp.

Location/Qualifiers

J. 376

Colone=Tykaoloffe

/clone=Tykaoloffe

/clone=Tykaoloffe

/clone=Tykaoloffe

/clone=Tykaoloffe

/clone=Tykaoloffe

/clone=Tykaoloffe

/de-stage="whole animal"

/de-stage="whole animal"

/de-stage="whole animal"

/de-stage="whole animal"
                                                                                                                                                                                                                                                                                                                                                                            C68576 Tuji Kohara unpublished cDNA Caenorhabditis elegans cDNA clone yk305f6 5', mRNA sequence.

C68576 C68576 G1:2429932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                          Gaps
/clone_lib="Yuji Kohara unpublished cDNA:Strain N2
hermaphrodite embryo"
/sex=hermaphrodite"
./dev_stage="embryo"
12 c 50 g 109 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%; Pred. No. 12;
Matches 19; Conservative 0; Mismatches 0; Indels
                                                                                                                                                            Query Match 1.3%; Score 19; DB 51; Length 360; Best Local Similarity 100.0%; Pred. No. 12; Matches 19; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: September 9, 2000, 21:38:20 Job time: 3143 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                 RESULT 15
C68576
                                                                                                                                                                                                                                                                                                                                                                                             LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
JOURNAL
COMMENT
                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE - AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           õ
                                                                                                                                                                                                                                                            δy
```

```
September 9, 2000, 20:17:02 ; Search time 1336.1 Seconds
(without alignments)
1926.152 Million cell updates/sec
                                                                                                US-09-214-679-1
1442
1 cccgggaactccatgtggcc.....aatgcaattcatttggatcc 1442
                                                                                                                                                                                         1945680
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                     972840 seqs, 892348106 residues
                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                       OM nucleic - nucleic search, using sw model
                                                                                                                                       IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                    9b_pr2:*
9b_rr3:*
9b_rr3:*
9b_sts:*
9b_sy:*
9b_un:*
em_tun:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     em_sy:*
em_un:*
em_vi:*
gb_htg1:*
gb_htg2:*
gb_in1:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         em_bal:*
em_ba2:*
em_hum3:*
em_hum4:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gb_pr4:*
gb_htg3:*
gb_htg4:*
gb_htg5:*
gb_htg6:*
                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 1000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            em_ph: *
em_pl: *
em_ro: *
em_sts: *
                                                                                                                                                                                                                                                                                GenEmbl:*
1: 9D_bal:*
3: 9D_bal:*
3: 9D_om:*
4: 9D_om:*
4: 9D_om:*
6: 9D_ph:*
7: 9D_pl:*
7: 9D_pl:*
9: 9D_pl:*
                                                                                                                                                                                                                                                                                                                                                                                  Title:
Perfect score:
Sequence:
                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                  Database :
                                                                                                                                                                     Searched:
                                                           Run on:
```

44: gp_htg7:* 46: em_htg3:* 47: em_htg3:* 48: em_htg3:* 49: gp_pl3:* 50: gp_pl3:* 52: gp_htg9:* 53: gp_htg9:* 54: gp_htg1:* 55: gp_htg1:* 56: gp_htg1:* 56: gp_htg1:* 57: gp_htg1:* 58: gp_htg1:* 58: gp_htg1:* 58: gp_htg1:* 58: gp_htg1:* 58: gp_htg1:* 59: gp_htg1:* 60: gp_htg1:* 59: gp_htg1:* 61: gp_htg1:* 62: em_htg7:* 64: em_htg2:* 64: em_htg2:* 65: gp_htg1:* 66: gp_htg1:* 67: gp_htg1:* 67: gp_htg2:* 67: gp_htg2:* 68: gp_htg2:* 69: gp_htg2:*	0: gb_htg3 1: gb_vi1: 2: gb_vi2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	A69475 Section 1		AP000059 Aeropyrum	AL132779 S.pombe c	AJ248285 Pyrococcu	AL162753 Neisseria	AC020050 Drosophil	AC008323 Drosophil	AC007420 Drosophil	AE003579 Drosophil	282196 Human DNA s	AE002546 Neisseria	AC015424 Drosophil	AC010003 Drosophil	AC009369 Drosophil	AE003521 Drosophil	I33795 Sequence 15	I33788 Sequence 6	U31226 Drosophila	AC013145 Drosophil	AL050231 Drosophil	AE003417 Drosophil	AL008609 Mycobacte	AL133507 Homo sapi
SUMMARIES	П	A69475	A72152	AP000059	SPAC869	CNSPAX03	NMA222491	AC020050	AC008323	AC007420	AE003579	HS288L1	AE002546	AC015424	AC010003	AC009369	AE003521	I33795	133788	DMU31226	AC013145	DMBR37P7	AE003417	MLCB1788	AL133507
	% Query Match Length DB	0 1442 5		16	0 35346 8	9 307120 1	9 349061 2	7 92918 43	7 123296 51	7 130583 41	7 304383 34	7 1	7 10619 2	7 133144 42	_	_	7 271237 34	vo	9 3900 5	6 3902 33	6 29692 42	6 102619 33	6 314661 34	5 39228 1	5 167306 32
•	% Query Score Match	1442 100.0	. ~		42.8 3.	41.2 2.	41.2 2.	39.6 2.	39.6 2.	39.6 2.	39.6 2.			39.2 2.	39.2 2.						36.8 2.	36.8 2.	36.8 2.	36.6 2.	36.6 2.
	Result No.	-		1 m	C 4	S	9 0	7	œ	σ	c 10	c 11	12	c 13	c 14	c 15	c 16	c 17	c 18	c 19	20	c 21	c 22	23	c 24

9	12	12	18.	18	24	24	30	30	36	36	42	42	48	48	54	54	09	09	99	99	72	72	78	78	84	84	06	06	96	96	102	102	108	108	114
qa	QY	qa	QY	qa	QY	qa	Qy	qu	QY	q	QY	qa	Qy	qu	Oy	đ	QY	qa	Qy	qQ	٥٧	ďΩ	δδ	qa	Oy	qa	QY	qa	οy	qa	QY	qu	QY	qa	Qy
AC002337 Arabidops AL020958 Streptomy		AJ276965 Phycomyce	ACUZ489/ HOMO Sapi ACU06759 Caenorhab	AL158134 HOMO Sapı AC025155 HOMO Sapi	X62629 D.melanogas	D32052 Oryza sativ AC013928 Drosophil			ABU33002 HOMO Sapi U96879 Arabidopsis	AKUZ9383 Sequence			OCCLARACTOR	00-M1-1999			Enterobacteriaceae;	11	ADIPOYL CEPHALOSPORINS								THHLTEEMQKEFHYTIGPYSTPV FLINPQNGPIMVNGAEKGDVLAVY	PLPEKVKMIKLDSEKVIWSKKHI IGPGSTITVLPVRAPGRLFIGDA	KMENAEN IMS 165AKFLEDATKI VDPKYTVGAMLNKNLLV"		Length 1442.		, C		
AC002337 SC4H8 AF200389	RNU55816	PBL276965	AC006759	AL158134 AC025155	DMLODE	RICMTNAD AC013928	AC016714	AC025648 AE003676			ALIGNMENTS		****	DNA nt W09802551.			eria; gamma subdivision;	T Complete State of the State o	BOVENDELY, R.A., Vall, D.L., Refinitely, R. and Mieller PROCESS FOR THE PRODUCTION OF ADIPOTENTE, WO 9802551-A 22-JAN-1998	) alifiers		a oxytoca	axon:571"	t=1	le=11 MIDASE"	protein_id="CAB42489.1" 'db_xref="GI:4760232"	/translation="MKWLBESIMARRGVGAGRKPVTHHLTEEMQKEFHYTIGPYSTPV LTIEPGDRIIVDTRDAFEGAINSEQDIPSQLLKMPFLNPQNGPIMVNGAEKGDVLAVY	LEYENLERGVDEYGLCAMLEHFGGLICOLLIAMLONDELPER WALKLUDERVYWERTHI LEYENLERGVDEYGLCAMLEHFGGLICOLLIAMLONDELPER WALKLUDERVYWERTHIOL LEYENLERGVGAMLANDEL TEATHER THE	HACQGGGETGGTAVEFASITITKVDLIKNWQLOWKKMENARNIMSIGSAKFLEDATKI AYRDITWLVEDFGFEQWDAYMLISQCGKVRLGNMVDPKYTVGAMLNKNLLV" 250 277 +	37 6 6 076	Score 1442. DR 5.	Pred. No. 0; Mismatches 0:	ostotadecence o, t	CONTROL	cogcacagogottgtgcggtaatggataaaaggccttgtttgtagaaacgctgacccaacaac
2.5 82592 49 2.5 15560 1	.4 5566	.4 2831	4 103725	.4 186808 .4 218096	4 4/39	.4 27588	.4 108964 .4 174208		3341	.4 5/33			6	1442 DP ce l from Patent	.1 GI:4760231	ella oxytoca.	ia; Proteobacteria;	ses 1 to 1442)	ED PROCESS FOF WO 9802551-P	BROCADES BV (NL) Location/Oualifiers	11442	/organism="Alebsiell /strain="PRS1" /icolate="PRS1"	/db_xref="taxon:571	/codon_start=1	/transl_table=11 /product="AMIDASE"	/protein_id /db_xref="C	/translatic LTIEPGDRIIV	LPYKPHIGTLS		ซ ก	100 08	larity 100.0%;	onservative	CCCCa Ly Lygocog (	cgctgtgcggtaat
25 36.2 26 35.8	35.2	35.25	33.3	35 35 35	34.6	34.6 34.6	34.6 34.6	34.6	34.4	34.2			-1	LOCUS A09475 DEFINITION Sequence ACCESSION A69475		THORES : URCE Klebsiella ORGANISM Klebsiella		REFERENCE 1 (bas					ŭ	cns					o c	BASE COUNT 36: ORIGIN	Ouerw Watch	Simi			
υc			o O					υ					A69475	DEFIN	VERSION	SOURCE	5	REFE	TIO	FEATURE									, ,	BASE	ā	M Be	2	<u>ک</u> ک	Z O

caccattggcccttattccacacccgtcctgaccatcgaacccggtgaccggattattgt agctetctgatgatettttaatgegtegteatetggetetgtaactaaaegetataaatt cgacactcgagatgcttttgaaggtgctatcaattcggaacaggatattccgagccagtt caatgatccgctgccagaaaaggtgcgcatgattaaactcgacagtgaaaaggtctactg tataggaccagggagtattacctatctgccggtacgtgcgcctggaggccgcctgtttat aattgcatatcgcgacttaatttactggctggtagaagactttggcttcgaacaatggga AATTGCATATCGCGACTTAATTTACTGGCTGGTAGAAGACTTTGGCTTCGAACAATGGGA acgtggagaataacatatgaaatggttggaagaatccattatggccaaacgcggtgttgg CGACACTCGAGATGCTTTTGAAGGTGCTATCAATTCGGAACAGGATATTCCGAGCTT 

us-09-214-679-1.rge

Db 61 CCGCACAGCGCTGTGCGGTAATGGATAAAGGCCTGGTTGTAGAAACGCTGACCAACAAC 120 Oy 121 agctctctgatgatcttttaatgcgtcgtcatctggctctgtaactaaacgctataaatt 180	181 acgtggagaataacatatgaaatggttggaagaatccattatggccaaacgcggtgttgg 24	Oy 241 tgccgggcgtaaaccggtaacgcatcacctgacggaagaaatgcaaaaagagtttcatta 300	Oy 301 caccattggccttattccacaccgtcctgaccatcgaaccggtgaccggattattgt 360	Oy 361 cgacactcgagatgcttttgaaggtgctatcaattcggaacaggatattccgagccagtt 420 	Oy 421 gctaaaaatgccctttctcaacccacaaaacggaccgatcatggtcaatggcgcggagaa 480	Oy 481 aggtgatgtgctgctgtctatatcgaatccatgttgcccgcggggttgatccctacgg 540	Oy 541 catctgcgccatgattccgcattttggcggactgaccggaccgacc	Qy         601 caatgatccgctgccagaaaggtgcgcatgattaaactcgacagtgaaaaggtctactg         660           Db         601 CAATGATCCGCTGCCAGAAAAGGTGCGCATGATTAAACTCGACAGTGAAAAGGTCTACTG         660 '	. Qy 661 gagcaaacgccatacgcttccctataaaccccatattggcaccttgagcgtatcgccaga 720	Qy 721 aattgactcaatcaattcactgacgccagacaatcacggcgggaatatggatgtgccgga 780	Oy 781 tataggaccagggagtattacctatctgccggtacgtgcgcctgagggcgcctgtttat 840	Oy 841 tggtgatgcccatgcttgtcagggtgatggtgagatttgcgggaccgcagtagagtttgc 900	Oy 901 ctcaatcaccaccatcaaagtcgatttgatcaagaactggcagctttcctggccacgaat 960	Oy 961 ggagaatgccgaaaatattatgagtattggcagtgcacgtccgctggaggatgcgacgcg 1020	Oy 1021 aattgcatatcgcgacttaatttactggctggtagaagactttggcttcgaacaatggga 1080	Oy 1081 tgcctacatgcttctgagtcaatgcggcaaagtgcggctgggcaacatggtcgaccccaa 1140	Oy 1141 atacaccgttggcgcgatgċtgaacaaaacctgttagtttagt
do Qy	da da	QY	Qy	QY	QQ Op	Qy	QY	QQ Dp	QY dg	Oy Og	Qy Db	QQ Dp	QQ Dp	VQ da	yo g	S G	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \
Db 1141 ATACACCGTTGGCGCGATGCTGAACAAAACCTGTTAGTTTAGTAGGAATAACTAAC	actcc 1	Oy 1321 ttcagcggagtgacggcacaagagttgtcacaatggcgcggagcaacccaggctatt 1380 	Oy 1381 gccgaaattaatcaaaatggcgcatcaacggcagaccactcaatgcaattcatttggat 1440 	Oy 1441 cc 1442 Db 1441 cc 1442	RESULT 2 A772152 A772157 1442 hn DNA DAT 11-MAY-1969	ITION Sequence 1 from Patent W09801568. SION A72152 ON A72152.1 GI:4808107	NERWOUSS . Riebstella oxytoca. SOUGANISM Klebsiella oxytoca Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;	ALEDSTRIAN. CE 1 (bases 1 to 1442) RS Brieden, W., Naughton, A., Robins, K., Shaw, N., Tinschert, A. an Zimmermann, T.	METHOD OF METHYLPROI L Patent: WC	FEATURES LOCATION/QUALITIERS  SOURCE 1. :1442  Organism="Klebsiella oxytoca"  Strain="PRS1"	/1solate="PKS1" /db_xref="taxon:571" 1971183 /codon_start=1	ASE. ASE. AB42722.1. 808108"	LTIEPGDRIYUDPA "KREADINA" KREÇOKREKYPYHHLEBMÜKEHYILGYSTPV LTIEPGDRIYUDPYEGAINESINAN KREÇOKREKYPYHHLEBMÜKEHYILGYSTPV LTIEPGDRIYUDPYEGAINEN KREÇOKREĞOKLIKMPELMEN KRENGOKREY KREY IESMLPRÇVDPYEICAMIPHFEGALGTATALFAMLNDPLPEKVRMIKLDSEKVYWSKRHY LISYKPHIGTLEVSYPEDIDSINSITIPDINGCIMDIYPDIGFOGTIYLEPYREGERLETEDA	HACGOLGELCCIAVERSITIINVULARNWULSHYKRENAESIIMSIUSAKPIEDAIKI ATRDLIYMLVEDFGFEQWDAYMLLSQCGKVRLGNMVDPKYTVGAMLNKNLLV" BASE COUNT 385 a 350 c 370 g 337 t.	Query Match Best Local Similarity 100.0%; Pred. No. 0; Matches 1442, Conservative O. Mismatches	cccgggaactccatgtggccgtgatcctggtcgagcaggatattgcgatgatccagcggg 60	61 ccgcacagcgctgtgcggtaatggataaaggcctggttgtagaaacgctgaccaacaac

q ŏ Op Ω

δŏ g δ Qγ

```
/codon_start=1
/transl_table=11
/transl_table=11
/product=1122a long hypothetical protein"
/protein_id="BAA79232.1"
/db_xref="G1:5103916"
/translation="MPGIERHSISVYAPRLFLVEVAGVLVRYLAPSIVERVLDAPSS
/vrinvlobrayFRIADAFIALAFGSRGADSYYLGLAKTLNEVATSDKVQAQNARKAGIK
SFYILSNNELEELMKYMGCK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /transl_table=11
/product="158aa long hypothetical protein"
/protein_id="88A79231.1"
/db_xref="G1:5103915"
/db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
/transl_table=11
/product="112aa long hypothetical protein"
/protein_id="BAA79229.1"
/boxtein_id="BAA79213"
/do_xref="01:5103913"
/translation="MRAGFIREEVDRRLVSLFEEFVDTGEAEAIVLAFERNAGLLL
MDDRDARNLAKKLGLQVMGTLGVIALAKYKGLTSKAKPIIDKLIESGFWISRRPLEEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MSLSIIGFALEVNPLYLANAITPSVPITCNPSFLARFLASRSI
SSKPALRSKARTIASASPVSTNSSKRDTSLLSTTSSTRIKPALTTFSLPGLPATVISA
QTVSGTRTSPKSFSRRSRRTLASAMIMLELETTRSLSSSSLLLCKLLGDLQILLQLL
                                                                                                                                                                                                                                                                                                                                                             /translation="METAIVYHLANKFHIPALAILGVSDYKAKNKVEFVTYEEELKDE
IFEIGLELTLEVK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(1152. .1490)
/gene="APE0276"
/note="similar to PIR:F69324 percent identity:47.115 in
104aa."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="similar to PIR:H69385 percent identity:39.175 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similar to PIR:F69385 percent identity:38.462 in
                                                                                                                                 to PIR:H71068 percent identity:29.167 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="164aa long hypothetical protein"
/protein_id="BAA79230.1"
/db_xref="GI:5103914"
                                                                                                                                                                                                        /transl_table=11
/product="57aa long hypothetical protein"
/protein_id="BAA79228.1"
/db_xref="G1:5103912".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(3301. .3669)
/gene="APE0279"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(3301. .3669)
/gene="APE0279"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(3752. .3979)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .2756)
                                                                                                                                                                                                                                                                                                                                                                                                                       complement(1152. .1490)
/gene="APE0276"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(2280. .2756)
.595)
                                                                complement(422. .595)
/gene="APES009"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="APE0278"
complement(2280.
/gene="APE0278"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="APE0277"
/gene="APE0277"
/1228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="APES010"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "APES010"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1228. .1722
/gene="APE0277"
                                                                                                                                    /note="similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                 /codon_start=1
/transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
                                     /gene="APES009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LRKLGESRNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene='
                                                                                                                                                                         48aa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
                    gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ultrect Submission

Submitted (14-DEC-1998) to the DDBJ/EMBL/GenBank databases. Yutaka Kawarabayasi, National Institutte of Technology and Evaluation, Biotechnology Center; Nishihara 2-49-10, Shibuya-ku, Tokyo 151-0066, Japan (E-mail:kyutaka@kazusa.or.jp, Tel:+81-3-3481-8951, Fax:+81-3-3481-8424)
Kawarabayasi, Y. is officially affiliated with the National Institute of Bioscience and Human-Technology, Tsukuba, Ibaraki 305-0046, Japan.
Nomura, N. and Sako, Y. are at Kyoto University, Sakyo-ku, Kyoto 606-8502, Japan
Nomura, N. and Sako, Y. are at the National Institute of Technology and The other authors are at the National Institute of Technology and The other authore with Hength 100 codons or more between ATG or GTG and stop codon are defined as CDS
Homology analysis is performed by Smith-Waterman algorithm against GenBank and GenBept release 109; EMBL release 56.0; SwissProt release 36.0; PIR-Protein release 57.0; and OWL release 31.0.
E-mail address for comments and questions: genomeAPPE@nite.go.jp
Restriction map, ORF organization, sequence alignment and more information are available at W.W.W. site of Biotechnology Center, URL: http://www.mild.nite.go.jp/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kawarabayasi,Y., Hino,Y., Horikawa,H., Yamazaki,S., Haikawa,Y., Jin-no,K., Takahashi,M., Sekine,M., Baba,S., Ankai,A., Kosugi,H. Hosoyama,A., Fukui,S., Naqai,Y., Nishijima,K., Nakazawa,H., Takamiya,M., Masuda,S., Funahashi,T., Tanaka,T., Kudoh,Y., Yamazaki,J., Kudoh,A., Oquchi,A., Aoki,K., Kubota,K., Nakamura,Y., Nomura,N., Sako,Y. and Kikuchi,H. Complete genome sequence of an aerobic hyper-thermophilic crenarchaeon, Aeropyrum pernix K1
DNA Res. 6 (2), 83-101 (1999)
                                        geegaaattaateaaaatggeggeateaaeggeagaeeaeteaatgeaatteatttggat 1440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Archãea; Crenarchaeota; Desulfurococcales; Desulfurococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 167000)
Tanaka,T., Hino,Y., Kawarabayasi,Y. and Kikuchi,H.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AP000059 167000 bp DNA BCT Aeropyrum pernix genomic DNA, section 2/7. AP000059 BA000002 AP000059.1 GI:5103911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Aeropyrum pernix"
/strain="K1"
/db_xref="taxon:56636"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aeropyrum pernix (strain:K1) DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pernix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aeropyrum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aeropyrum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (sites)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cc 1442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1441 CC 1442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 3
AP000059/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GRGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                    1261
                                                                                                                                                                                                                                                                                                                                                                                  1321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
TITLE
                                                                                                                      1201
                                                                                                                                                                                   1261
                                                                                                                                                                                                                                                                                                                     1321
                                                                                                                                                                                                                                                                                                                                                                                                                                               1381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                         1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               q
```

```
/LTANSIAL 1018—WOOHROORMSRELIGLGAGILIRLLLKNLKKKGQHIEERAPPO
LTREGIDOYIYDTTIDEAYEQLQAFYDRAYRELLKREKEABEDPHIKKLIQNIKEYHEL
FRYDNEMR PPWALTTIDEAYEQLQAFYDRAYRELLKREKEABEDPHIKKLIQNIKEYHEL
FRYDNEMR PPWALTAILLBALKHGVKDRDK IYQYILKASWEYAKEIAGALPAKKYGG
RYTRAYADQWRNPFISIEIEAMIRBANRDDPKWKKYTOWFDLYWMKIPDDIYNRADS
OHHEVTKYLQLLEFALREAERESGVBPFWHKTPEETILGIGFGEGPAPAGEPILAYPDR
KGRHYSPLYOLLGALKFULGEFREGGGYHEDLYRTDLAYPTTHHWYPERLEBNEE
KGRHYSPLTOLLQALKPWPELKORAYRYLAGIEGOKSISEIPEEERKAFREVIERLK
EIWRNPDRFVPIVEELYATGMNIKDAAKTLIGVLDDFAKIYSGEKSPRQAGIERDAT
OLYNTYKRARDRGNYUPPYHTBLINIIEQHDPLIKARYPEETEBEBKAFREVIERLE
OLYNTYKREBEEEKKLGIEGERKKKLSEGDIRRTAMIYRTLAFPHPSLEDIKR
FYSRLAERVVEEEREEKKLGIEGERRWKLSEGDIRRTAMIYRTLAFPHPSLEDIK
/product="75aa long hypothetical protein"
/protein_id="RAA79233.1"
/db_xref="G1:5103917"
/translation="WalerryEigmskVIRVRYERGVLKPLEPVNLEDGEEVDIIIREN
LAELARRIRRRLSQEREEPSEILSRERSRLA"
                                                                                                                                                                                                                                                                                                                                                /product-"108aa long hypothetical protein"
/protein_id="BAA79235.1"
/d_xref="G1:510489235.1"
/translation="WTHPPTVTUSPMMTSSVGVMRWAGTVPAGNNATEHTAVPAISO
SSFDSFFTCASRTS1AASSAVVSALPPTPFATILTSSTKLLYIGLYFSSPHDKIRKAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MSSGILFQYRSNICVYFFHFGSSLFASLIIASISMIDIKGFLIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAYARVYLPWYFLAGRACAISFAYSQLAFRMYWYILSLSFTPCFRASFSRIAVSIQGG
LISLSFLNSSWYSFWFCMSFLMWGSSASFSLFRSSRYALSYSACSCSYASSIVVSTMY
WSICSRVSWGGALSSMCCPFFLRFLSRSRMSMPAPRPISSLLILPSPLWSPIQRLPCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="APE0283"
4831. .6840
/gene="APE0283"
/note="motif-ATP/GTP-binding site motif A (P-loop)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FHAAPHIKEGVMSVLAATRSNIVSGEKHEEFIRHLERTQVRRPLE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="669aa long hypothetical protein"
/protein_id="BAA79237.1"
/db_xref="61:5103921"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
/transl_table=11
/product="102aa long hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /transl_table=11
/product="220aa long hypothetical protein"
/protein_id="BAA79236.1"
/db_xref="G1:5103920"
                                                                                                                                                                                                                                             /codon_start=1
/transl_cable=11
/product="124aa long hypothetical protein"
/protein_id="BAA79234.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(4803. .5465)
/gene="APE0282"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(4803. .5465)
                                                                                                                                                                                                                                                                                                                                                                                                                                          MVRVALEGGLSIVGIDMEGDLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(4516. .4842)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(4516. .4842)
/gene="APE0281"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(5360. .5668)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(5360. .5668)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_table=11
                                                                                                                                       1028. .4402
/gene="APE0280"
                                                                                                                                                                                          4028. .4402
/gene="APE0280"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="APE0281"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="APE0284"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="APE0284"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="APE0282"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .6840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KRQMAP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4831.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene
                                                                                                                                          gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
```

```
WELL, http://www.sanger.ac.uk/Projects/S_pombe/)
Luring 1995 to 1996 about 66% of S. pombe chromosome 1 was
During 1995 to 1996 about 66% of S. pombe chromosome 1 was
sequenced by the Sanger Centre. The sequencing of the S. pombe
genome is now being continued with funding from The European
Commission. Fourteen Buropean sequencing laboratories, including
the Sanger Centre, are participating in the project.
Protein coding regions (CDS) have been predicted with the help of
computer analysis using the Genefinder program in PomBase (an ACEDB
database) with additional predictions for the branch-acceptor sites
supplied by the program 8538plice. CAUTION: It is possible that for
any individual CDS we may have underestimated or overestimated the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alpha-galactosidase; amidase; amino-acid permease; flavohemoprotein; formamidase; globin; oxidoreductase; protein-1-isoaspartate o-methyltransferase; sodium:solute symporter family; sulfate permease; sulfate transporter family; TFI LTR; urea active transporter.
/protein_id="BAA79238.1"
Abaxref="01:5103922"
/translation="MGGTCPGRRVSALPPARDPLPVLCRGFPRGSCARRALPPIPFLP
HEGPLPGVAGILLLHDAASRPYYRCRPESCSNTDQTSVYIFSTSDHPCILLLSSPRFL
                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jebelsone. SP (S. .01 (first CDS), c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hunt.C., Aves.S., McDougall,R.C., Rajandream,M.A. and Barrell,B.G. Direct Submission
Submitted (02-NOV-1999) European Schizosaccharomyces genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and Department of Biological Sciences, University of Exeter, Perry Road, Exeter EX4 4QG, United Kingdom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Notes:
Details of yeast sequencing at the Sanger Centre are available on
                                                                                                                                                                                                                                                                                                                                                                                                                                                  161764 TCGTCGAGGGGCGCTATTCTCGGTGGGCGACGCCACTATGCCCAGGGCGAGG 161705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161824 ACGGAGGAAACCTCGATGTGAGGCACTTCTCCCCAGGCTCCAAAATCTACTTCCCCGTGT 161765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (complementary strand). The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                816 gtgcgcctggaggccgcctgtttattggtgatgcccatgcttgtcagggtgatggtgaga 875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  876 tttgcgggaccgcagtagagtttgcctcaatcaccaccatcaaagtcgatttgatcaaga 935
                                                                                                                                                                                                                                                                                              756 acggcgggaatatggatgtgccggatataggaccagggagtattacctatctgccggtac 815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         number of introns/exons or we may not have chosen the correct splice donor/acceptor sites.
CDS are numbered using the following system eg SPBC25H2.0lc.; pombe), B (chromosome 2), c25H2 (cosmid name), .01 (first CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    On Dec 16, 1999 this sequence version replaced gi:6224591.
                                                                                                                                                                                                                                   ö
                                                                                                                                                                         Length 167000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales;
Schizosaccharomycetaceae; Schizosaccharomyces.
                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLN
                                                                                                                                                                                                                                87;
                                                                                                                                                                         1;
                                                                                                                                                                      Score 45.8; DB
Pred. No. 0.07;
                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35346 bp DNA chromosome I cosmid c869.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL132779
AL132779.2 GI:6594223
                                                                                                                                                                      3.2%;
                                                                                                                                                                                                                                   98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fission yeast.
                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 161644 AGGGG 161640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    936 actgg 940
                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPAC869/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOURCE
                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
```

gene

FEATURES

```
/product="hypothetical protein"
/product="hypothetical protein"
/product="hypothetical"
/product="file"CAB60016.1"
/db_xref="d1:6224597"
/translation="MLQYSKKKVSLNEFPVRLLSYKMTRISDAIFKDHRKLQSDYONI
/translation="MLQYSKKKVSLNEFPVRLLSYKMTRISDAIFKDHRKLQSDYONI
/ksandydpatrangongrwaelahasygeretyvpkfekyfekyfekyfekylsheseselhanassferialion="manage"
BRTKRFPHSHRSAPNKPPFETVAGLFAAPIDKLRDMMEKWP"
16383, .18905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(8783. .9427)
/gene="SPAC869.08"
/gene="SPAC869.08"
/note="March to PF01135 PCMT,
Protein-1-isoaspartate(D-aspartate) O-methyltransferase
(PCMT) Score 263.14"
/l0265. .11575
/gene="SPAC869.07c"
/10265. .11575
/gene="SPAC869.07c"
/note="SPAC869.07c"
/note="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="putative alpha-galactosidase"
/product="putative alpha-galactosidase"
/product="caractive alpha-galactosidase"
/db_xref="G1:6224598"
/db_xref="G1:6224598"
/db_xref="G1:6224598"
/db_xref="G1:6224598"
/db_xref="G1:6224598"
/db_xref="G1:624598"
/db_xref=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FSRKDYRCPCTTIECTALGOHCSVANTISKASELSSKAGMNSGNNDLDSLEVGNGGM
SPEETYRHFTGTALGOHCSVANTISKASFLSSKAGMNSGNNDLDSLEVGNGGM
SYEDEYIEFFWAILKSPLILGNDVSNSSMSPPMKLIVSNKELISINQDIGTURAALIWK
KKYGDEYIEFFSGRISKASNNDWVVAVLANASEPLKMGIHLSDIFVDALGNAEHDMLATDL
WNNNYKLVSDRIRRANVASHGVQWRFQQYKVKNTNDKFFSFNKH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="CAB60018.1"
/db_xref="G1:6224599"
/db_xref="G1:6224599"
/translation="MRWSFNLSSNAALVQHLVESKFLTNQRAIKAMNATSRSFYCPLS
/translation="MRWSFNLSNAALVQHLVESKFLTNQRAIKAMNATSRSFYCPLS
/translation="MRWSFNLSNAHMATALQELEPYLQPGCSALDIGSGSGYLVAANARWVAP
NGTVKGIEHIPOLVPESKKNLIKDINHDEVLMEMYKEKRLQINVGDGRMGTSEDEKFD
AIHVGASASEEPPQKLVDQLKSPGKILIFPIGTYSQNIYLIEKNEQGKISKRTLFPPVRYV
                                                                                                                                                                                                                                                                                                                                                                                         /product="hypothetical protein"
/protein_id="CaB60019.1"
/db_xref="G1:6224600"
/db_xref="G1:6224600"
/translation="MPDPAHIIAGHKAALSNPHVSEEAKERARKYLKEHGSESHYTTG
TYRGQKADDAGELREEGFGTKNQFEDNESQAKNLGNVRGGYKAAMHNPKVSQKGRR
HAKELLEEVDDESK"
complement(8756...9448)
                                                                                       /note="SPAC869.09, len:116, SIMILARITY:Schizosaccharomyces pombe, YAAB_SCHPO, hypothetical 15.4 kd protein c2297.11c in chromosome i., (140 aa), fasta scores: opt: 192, E():2.5e-06, (39.6% identity in 139 aa)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(8756..9448)
/gene="SPAC869.08"
complement(8756..9448)
/gene="SPAC869.08"
/gene="SPAC869.08"
/note="SPAC869.08, len:230, SIMILARITX:Triticum aestivum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PINT_WHEAT, protein 1-isoaspartate o methyltransferase, (230 aa), fasta scores: opt: 602, E():2.2e-32, (48.5% identity in 200 aa)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="putative protein-l-isoaspartate o-methyltransferase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="SPAC869.06c"
/note="SPAC869.06c, len:203"
complement(7524..7874)
/gene="SPAC869.09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="SPAC869.06c"
13058. .13669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
/label=SPAC869.07c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label=SPAC869.06c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label=SPAC869.08
                                                                                                                                                                                                                                                                                                                                                              /label=SPAC869.09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                                             /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PLTDSPDDSSDY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                     CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="amino-acid permease"
/product="amino-acid permease"
/product="amino-acid permease"
/procein_id="CAB60021.1"
/db.xref="G1:6224602"
/translation="MEPEYVSFSDKDTKSILNESKSSLKDVKPSLEEKSTITPGLVDD
/translation="MEPEYVSFSDKDTKSILNESKSSLKDVKPSLEEKSTITPGLVDD
/translation="MEPETYARJGEMAYAYPAGGFNIYATFIDPAGFAVSW
LADGGPASVIINYSLIGIMMFFIVYALGEMAYAYPAGGFNIYATFIDPAGFAVSW
NYFINYFWFPDELETTCAITFRYWDINISAAMISIFLVVYIIVNLFGVRAYGEVFFILL
STYKVVATFGFIILALIIAALINGGVPPDHGXIGGSIKHKPFRGFEGSVFTTAAFS
FKYTDRIGNELLAABVKGLPVFNAVIIISVSTYNSSTTAGFTHGMANLKGAPSF
FKYTDRIGNELLAAMIVVLLEFFFAXINBADKNGNDVSDTVFNWLLALSGLSNFFTWGS
ICLCHIIFRLAFKKQGHSLKELGFVSPMGINGSCIGLFFNILCLAAQFYVSLFPIGGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              //Jabel=SPAC869.10c
/product="amino-acid permease"
/product="amino-acid permease"
/protein_id="CAB60020.1"
/bcrein_id="CAB60020.1"
/bcrein_id="CAB60020.1"
/translation="MDEKRALQYEESKRAEEITDIELVSVGGIDVEKKYGETKRALKS
/translation="MDEKRALQYEESKRAEEITDIELVSVGGIDVEKKYGETKRALKS
RHVQLIAIGGCIGTGLFVGSGSALSESGPASLFLSYVIMSTVIMIALGERVTYLP
ILGASPITYERXVDASLAFAAGWNYMYATVPELVASEVTAASIVIEYWTYAVPTAGWI
ALLELVAVLNSFFVKWFGETEFWFALIKVALVGHILIGYVIFFGGTPKHDRLGFRY
WKHGLAFREY IVKGGSGRFVGFWSAVLKSGFAFILAPELVIFFSAGETEAPRRUIPKAT
SRFIYRLIFFYIFGSLTIGVITSSKDPRLLMALSSASGFAFILAPELVIFSAGETEAPRRUIPKAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="SPAC869.10c, len:552, SIMILABITY:Emericella
nidulans, PUTX_EMENI, proline-specific permease, (550 aa),
fasta scores: opt: 1968, E():0, (53.3% identity in 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HIINAVILTSACSSGNSFLEAGSRSIYSLAKEHQAPKIFKYCRKWGVPTISVAVTVLF
ACLAPLNASASAAVVENWFCNISTISGFLAMICVLVAVLQFRKAMILNNLWETRPYKT
PFQPYATYLTLFLLALITLTNGFTVFVGHTFTAGNFIAAXITLPIFLVLXVAHKLWSR
NWSFGKRIEEIDVTTGVAEABALEQMYPAPVPRNIIEKIWFWIA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="SPAC869.11, len:536, SIMILARITY:Schizosaccharomyces pombe, ISP5_SCHPO, sexual differentiation process putative amino-acid permease isp5., (543 aa), fasta scores: opt: 1812, E():0, (53.9% identity in 492 aa)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3816. .5228 // Agene="SPAC869.10c" // Amote="Match to PF00324 aa_permeases, Amino acid permease Score 718.22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(3. .1394)
//gene="SPAC869.11"
/note="Match to PF00324 aa_permeases, Amino acid permease Score 820.26"
3705. .5363
          IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Overlap with c922 S. pombe chromosome 1" complement(1. .1610)
                                                                                                                                                                                                                                                                                                             /organism="Schizosaccharomyces pombe"/strain="972h-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (6788. .7138)
/note="TF1 LTR"
complement (7524. .7874)
/gene="SPAC869.09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:4896"
/chromosome="1"
/clone="cosmid c869"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3705. .5363
/gene="SPAC869.10c"
3705. .5363
/gene="SPAC869.10c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(1. .1610)
/gene="SPAC869.11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="SPAC869.11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label=SPAC869.11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /map="IR"
complement(1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /partia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
```

gene

CDS

gene

LIR

```
/transl_table=11
/product="hypothetical protein"
/product="hypothetical protein"
/protein_id="CAB49560.1"
/db_xref="el-858071"
/translation="MSYYDEYLDNLKGWRIRKALEIVREKKEEKLEVIKRALQEKDPL
/translation="MSYYDEYLDNLKGWRIRKALEIDDRDESYVLQTVETINAINFMDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MRVSLDEIDRRIIKILQKDGKAPLREISKITGLAESTIHERIKK
LRESGVIRKFTAIVNPEALGYSMLAFILIKVKAGKYAEVASNLVKYEEIMEVYETTGD
YDMVVKIRTKNSEELNSFLDVIGSIPGVEGTHTMIVLKTHKETTELPIK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product-"snRNP, putative"
/protein_id="CAB4958.1"
/db_xref="GI:558074"
/translation="MAERPLDVIHRSLDKDVLVILKKGFEFRGRLIGYDIHLNVVLAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EQHMAVLELAKSDYKVLQLVIRIFLSEDLLTKLDALWVISNATSYIKIDDAMKIIPQL
EEFLLHYNPWVRSTSAKVLADLALEYSSIMEREISKALELIESNDEKLVIAGIELADA
LLSRIKNIGFLREVMKRLIRKDRLPREALDFIKKYESYIEELEPEIKRQISIKLVNSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /transl_table=11
/product="transcriptional regulatory protein, AsnC family"
/protein_id="CA849562.1"
/db_xref="G1:5458073"
                                                                     /translation="MKVIKEWNVKVKLVRTKRGAILHMIELKPGHFFLEQNPLKPSKY
GEAYRKIKQNFPEFYFFWEIKDNKYTGRILAGAFLEKEEIDEFLTLLAKTEDFKKLEH
                                                                                                                                                                                                                                                                                                                                                                       /translation-"MMPMNPKQLKKLMKQLDMKQLDGVKEVIIKLENKEIVIKEPVVT
VIRAMGEKMYQIAGGTEEERVVLKISEEDIKLVMEQAGVDYETAKKALEEAGGDLAEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KKKVSALRVLREIVTRTKNEKIMEBAFNLALDVLNDEDPVVRSTALKIIEVAIDRREF
LSRESLEKASAMLGSSSIGKETKEKIDEILQGREEKKVKTEVSVKDYSVEIIKEMFER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEDLSSELSDVLIGIVENKPEPINEYAAEGVATLGAKIIMIARKIFSWIRGILQGKST
                                                                                                                                                                                           /anticodon=(pos:601906. .601908,aa:Leu)
1674. .2003
/note="PAB0439"
      /product="hypothetical protein"
/protein_id="CAB49558.1"
/db_xref="GI:5458069"
                                                                                                                                                                                                                                                                                                        /product="hypothetical protein"
/protein_id="CAB49559.1"
/db_xref="GI:5458070"
                                                                                                                                     1570. .1656
/note="codon recognized: AAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(3344. .4747)
/note="PAB1939"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(4815..5270)
/note="PAB1938"
                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(1983. .3347)
                                                                                                                                                                              /product="tRNA-Leu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5407. .5634
/gene="snrnp"
5407. .5634
/gene="snrnp"
/note="PAB8160"
                                                                                                                                                                                                                                                                  /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="PAB1940"
                                                                                                                 VLEEIEEIEEGEE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                 ILRLTDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VGEP"
                                                                                                                                     trna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MVNYELLKKVVEAPGVSGYEFLGIRDVVIEEIKDYVDEVKVDKL
GNVIAHRKGEGRKWIAAHMDQIGLMYTNIERNGFLRVAPIGGVDPKTLIAQRFKVWI
DKDKFIYGVGASVPPHIQKPEERKKAPEWDQIFIDGAESKEEAEEMGVRIGTYTWD
GRLEIVGKHRYSIAPDDIAVYTMYSTAVDAVARQLEDTKADVYFVATVQEEVGLKGARTSA
FAIEDDYGFAIDVIAADVPGFPEHKQVTHLGKGTAKIMDRSVICHPIURWLEELA
KKYEIPYQLEILLGGGTDAGAIHLTKAGVPTGALSVPARIHSNAEVVDERDVDATVK
                                                                                    SMILARITY:Schizosaccharomyces pombe, SULH_SCHPO, probable sulfate permease spbc3h7.02., (877 aa), fasta scores: opt: 3127, E():0, (62.8% identity in 827 aa)"
                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (06-001-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
                                                                                                                                                                                                                                                                                                                                                                                                             22212 CAAGGACAATACCGGGGAGACCCGAAAATGGAGAAATTGCGATATTAAAAATTTATCAA 22153
                                                                                                                                                                                                                                                                                                                               caatcaattcactgacgccagacaatcacggcgggaatatggatgtgccggatataggac 788
                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence: insights into archaeal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pyrococcus abyssi.
Pyrococcus abyssi
Archaea; Euryarchaeota; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                            Length 35346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
/transl_table=11
/product=aminopeptidase from family M42"
/protein_id="CAR49557.1"
/db_xref="G1:5458068"
                                                                                                                                                                                                                                                                                  67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genome; segment 3/6.
                                                                                                                                                     /codon_start=1
/label=SPAC869.05c
/product="probable sulfate permease"
                                                                                                                                                                                                                                     Score 42.8; DB 8;
Pred. No. 0.39;
0; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 .307120
/organism="Pyrococcus abyssi"
                          16383. .18905
/gene="SPAC869.05c"
/note="SPAC869.05c, len:840,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  849 cccatgcttgtcagggtgatggtgagattt 878
||| || || || || || || || || 22092 TTCATTTTCTCAAGGTGATGGCGAAATTT 22063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pyrococcus abyssi genome sequence: chromosome structure and evolution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="Orsay"
/db_xref="taxon:29292"
98. .1144
/gene="SPAC869.05c"
16383. .18905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CNSPAXO3 307120 bp DNA
PYCOCCUS abyssi complete
AJ44285 AL096836
AJ24285.1 G1:5458067
complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="PAB0437"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1188. .1535
/note="PAB0438"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LMVKALENIHELKI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 307120)
Heilig, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 307120)
                                                                                                                                                                                                                                        3.0%;
illarity 55.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pyrococcus.
                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genoscope.
                                                                                                                                                                                                                                                                                  83;
                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                                                                                                                            729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CNSPAX03
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
                             CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOURCE
```

Ob

g δ

ò qq ò

gene

CDS

CDS

```
/product="hypothetical protein"
/product="hypothetical protein"
/product="hypothetical protein"
/db_xref="G1:5458080"
/dranslation="mxkwrkyrvyrpteintarkyryryratakaasg
byssytriskemkkoigrdwrehegevyvyrpteintarkyryryryrdd
krkklefaligalkkabelgyrsiafpalsagiygcpleevyktfklyvneflksakn
ytdyylvlysbendyrbalkylerdel"
                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="ATR repeat; humis hit to HMM ATR (1 - 183), score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 282150 TACTICCCIGICITCGITGARGAGCTTACCICGCIAIAGGGGAITTGCAIGCCGIAAIG 282209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NMA222491 349061 bp DNA BCT 30-MAR-2000 .
Neisseria meningitidis serogroup A strain 22491 complete genome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Parkhill, J., Achtman, M., James, K.D., Bentley, S.D., Churcher, C., Riee, S.R., Morelli, G., Basham, D., Brown, D., Chillingworth, T., Rale, S.R., Morelli, G., Basham, D., Brown, D., Chillingworth, T., Handles, R.M., Davis, P., Devlin, K., Feltwell, T., Hamlin, N., Holroyd, S., Jagels, K., Leather, S., Moule, S., Mungall, K., Quail, M.A., Rajandream, M.A., Rutherford, K.M., Simmonds, M., Skelton, J., Whitehead, S., Spratt, B.G. and Barrell, B.G. complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Details of N. meningitidis sequencing at the Sanger Centre are available on the World Wide Web.

(URL, http://www.sanger.ac.uk/Projects/N_meningitidis/).

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                      743 acgccagacaatcacggcgggaatatggatgtgccggatataggaccagggagtattacc 802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      862
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (30.MAR-2000) Submitted on behalf of the Neisseria
sequencing team, Sanger Centre, Wellcome Trust Genome Campus,
Hinxton, Cambridge CB10 1SA E-mail: parkhill@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      803 tatctgccggtacgtgcgcctggaggccgctgtttattggtgatgcccatgcttgtcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria meningitidis
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae;
                                                                                                                                                                                                                                                                                                                                   th 2.9%; Score 41.2; DB 1; Length 307120; Similarity 53.8%; Pred. No. 1.8; B5; Conservative 0; Mismatches 73; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. ,349061
/organism="Neisseria meningitidis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 282210 GGAGATGCCGAAGTCTGCGTCTCGGCTTGTGAGGTTTC 282247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         863 ggtgatggtgagatttgcgggaccgcagtagagtttgc 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 404 (6777), 502-506 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:487"
/note="serogroup: A"
complement(24. .206)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="Z2491"
                                                                                    /transl_table=11
      10500. .11060
/note="PAB0445"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neisseria meningitidis.
                                                            /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          segment 2/7.
AL162753 AL157959
AL162753.2 GI:7379120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 349061)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    310.39"
/label=ATR
209. .212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Parkhill, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20222556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Notes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_unit
                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
NMA2Z2491/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
               CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ōλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="CAB49567.1"
/protein_id="CAB49567.1"
/db_xerf="C1:5458078"
/db_xerf="C1:5458078"
/db_xerf="C1:5458078"
/db_xerf="C1:5458078"
/db_xerf="C1:5458078"
/db_xerf="C1:5458078"
/db_xerf="WYSLSYULRGGIVLYGRDYKLTRADVLIEGDKIVEVKRNINKPA
/translation="WYSLSYULRGGIVENEDFARAPEEDVPLMEWLQEYIMPVERKIRKRODYW
GSKLALIEMAHGGTGTETPUMYFHMEETARAPEEDVPLMEWLDGETIGRKRIEMR
GSKLALIEMAHGGTGTGTFPUMYFHMEETARAPETGGINSERGREWNSLUTTHLAETQDB
FTIRKYGKSPUVDVEDVOGLINEKLIAAHGTWLSDEDIRKISSAGATTAHCPASNMK
IGSGVFPMKRALENNYNVALGTDGAASNNTLDILREMRLASLLQKVIHRDPSIVKSED
IFRMATUNGARALGLAGAGVIAGSTADIAVIDLRKAHLLPVNSPLASIIFSARGGDVD
TLIVGGEIVWLDSELLTVDEEKVIDKFLEVSVA"
/note="PAB0444"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cougli_table=11
/product="hypothetical protein"
/product="hypothetical protein"
/product="hypothetical protein"
/product="hypothetical protein"
/product="hypothetical protein"
/do_xref="di:5458076"
/translation="mslealFnPKSIaVIGASSKPGKIGYAIMKNLIEYGYBGKIYPV
/kranslation="mslealFnPKSTIAVIGASSKPGKIGYVYPERGGGGGKKVVPIIS
/kranslation="mslearkystiavigastropergokvVypaklingtropergokvVvPIIS
/kranslation="mslearkystiavigastropergokvVvIpaklingtropergokvVvPIIS
/kranslation="mslearkystiavigastropergokyvVilingtogramatharegoksgg
/kranslaticastropergokvVvIntropergokvVilingtogramatharegoksgg
/kranslaticastropergokvVvIvAIvGGIEAKEAIDTLNENGIPAYPEPERRAVKALSALY
/kranslatingtogramatharegoksggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MIPPFKEVLMGIPPLVIYVVLFYHYIISRNSSYLMYFSLAFLSL
GVGIMVEDAYLAGLAFFSSFFWIGVIQFLRRLGGFKGLNLKXLLYVAPTSLASYMFFL
BNSBYTILVFYYSLMATLIAIMLAFKYKTSYFYLLLVAVYSVEGYYSDLAKYLFYIIA
TTLGYFLILVFTKIDLRYTILSPPSTGEELKLRPGVIFAETIPBDILKVALFSKRYGK
GERWFWYTKLKSSDWYNIEPPRNLPKILSLAVDYLKKKGVVVIDCLDYLILENGFESVI
KFMAHLRDYAVMHGSSVIILGPLEGLSDKEKVMLKRRGVVVIDCLDYLILENGFESVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xrei="u.: a. a. bu//
/translation="WYGMLEVNLFGIKFKNPLILASGVVDMTPELLRRAHREGAGGV
/translation="WYGMLEVNLFGIKFKNPLILASGVVDMTPELLRRAHREGAGGV
/translation="WYGMLEVGILNAMGLDNPGREAFLEEFRKEKFDFPVIVSIFG
GTPEEFAFLAEKLGEVADAFELNLSCPHAKGYGMEIGGKPENYYEVKAVKDVIVSIFG
GTPEEFAFLAEKLGEVADAFELNLSCPHAKGYGMEIGGKPENYYEVKAVKNOYTDKPV
IARLTPNYNDIASSLDIPVIGIGGITYWQDAVSINIVKAIALDITAKRPILSNKFGGYSGPV
IARLTANYDLASSLDIPVIGIGGITYWQDAVEFLLAGASALQIGTAVYLRGFSVFRE
IARGISRYLKEGGYSSVKEIIGLALKV"
/gene="neac"
/gene="neac"
/gene="neac"
/gene="neac"
                                                                                                                                                                                                                                                                                                                          /translation="MSSGTPSLGKRNKTPTHIRCRRCGRKAFNVKKGYCAACGFGRSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transl_table=11
/product="dihydroorotase dehydrogenase (pyrD)"
/protein_id="CAB49566.1"
/db_xref="G1:5458077"
                                                                                                                                                                                                          /transl_table=11
/product="LSU ribosomal protein L37E (rpl37E)"
/protein_id="CAB49564.1"
/db_xref="G1:9458075"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transl_table=11
/product="chlorohydrolase, putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="hypothetical protein"
/protein_id="CAB49568.1"
/db_xref="G1:5458079"
AEMIQDGEVVKRYGKIVIRGDNVLAISPTEE"
5646. .5834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(7322. .8233)
/note="PAB1936"
                                                                                                                                                                                                                                                                                                                                                                                         complement(5846. .7228)
/note="PAB1937"
                                                                                                                                                                                                                                                                                                                                                                    RLRKYRWSKKWKKKKNVH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="PAB0443"
                                                                                                                                                                /note="PAB7160"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
                                                   5646. .5834
/gene="rpl37E"
                                                                                                            5646. .5834
/gene="rpl37E"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RWSKWKAKHK"
```

gene

CDS

```
Jobes NAMA0373, thif, probable Thir protein, len: 256 aa, similar to e.g. THIF_ECOLI P30138 THIR protein (251 aa), fasta scores; E(): 0, 43.1% identity in 246 aa overlap, and MOBB_ECOLI P1282 molybdopterin biosynthesis MOBB protein. (249 aa), fasta scores; E(): 0, 43.9% identity in any other molybdopterin biosynthesis protein. E(): physography of the protein plantity in any other molybdopterin biosynthesis proteins). Contains pram match to entry PF00899 Thir_family, Thir family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="fhire protein"
/protein_id="CAB83674_1"
/db.xref="G1:7379124_1"
/db.xref="G1:7379124_1"
/db.xref="G1:7379124_1"
/db.xref="G1:7379124_1"
/db.xref="G1:7379124_1"
/db.xref="G1:7379124_1"
/db.xref="G1:7379124_1"
/dranslpxtransgrightsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproteinsproproteinsproproteinsproteinsproproteinsproproteinsproproteinsproproteinsproproteinsproteinsproproteinsproproteinsproproteinsproproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsproteinsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="NMA0374, ppc, phosphoenolpyruvate carboxylase, len: 917 aa: simlar to many e.g. CAPP_RHOPA 032483 phosphoenolpyruvate carboxylase (EC 4.1.1.31) (936 aa), fasta scores: EC(1: 0, 43.3% identity in 928 aa overlap. Contains 2x Pfam match to entry PF00311 PEPcase, phosphoenolpyruvate carboxylase, PS00017 AFP/GFP-binding site motif A (P-loop), and PS00393 Phosphoenolpyruvate carboxylase, active site 2"
/note="NWA0371, slyX, SLYX protein homolog, len: 74 aa; simlar to SLYX HAEIN P44759 SLYX protein homolog (73 aa), fasta scores; E(): 0.0017, 33.8% identity, in 74 aa overlap, and SLYX_ECOLI P30857 SLYX protein (72 aa), fasta scores; E(): 0.24, 32.4% identity in 68 aa overlap"
                                                                                                                                                                                                                                                                        /product="SLYX protein homolog"
/protein_id="CABB3672.1"
/brotein_id="CABB3672.1"
/bc_xref="G1:7379124"
/translation="MANVQEFERITELEIQSALQEDVIAGLNAWVAELRQTLDLQQAQLRLLYQKMQDRNPDAQEPYSLRDEIPPHY"
/complement[327]. .3423)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MFGRLSPLGSDGFFLAVYEYPVGFICLQGKTAYFRSGGKRFHRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aa 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Pfam match to entry PF00899 Thir_family, Thir family, score 186.60, E-value 4.1e-52" complement(4418. .4427)
/note="Core DNA uptake sequence: gccgtctgaa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(3271. .3423)
/gene="NWA0372"
/note="NWA0372, unknown, questionable CDS, len: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3787. 3796
/note="Core DNA uptake sequence: gccgtctgaa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
/transl_table=11
/product="very hypothetical protein NMA0372"
/protein_id="CAB83673.1"
/db_xref="GI:7379125"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KGILSD"
1356.. 3571
/hote="Core DNA uptake sequence: gccgtctgaa"
/label=DUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label=Dus
complement(3847. .4257)
/gene="thif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(3586. .4356)
/gene="thif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(3586. .4356)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /EC_number="4.1.1.31"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
/transl_table=11
                                                                                                                                                                                            /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="NMA0372"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="thiF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="ppc"
4471.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4471. .7224
/gene="ppc"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label=DUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /transl_table=11
/product="HemK protein"
/product="HemK protein"
/product="HemK protein"
/db xref="d1",379122"
/translation="MTFDKWLGLSKLPKNEARMLLOYVSEYTRVQLLTRGGEEMPDEV
RSADARLAGGRRINGEPVAY LIGAREFYGRRFYWDSVLLFRPETEHLYBAYLARLPEN
GRAWDLAGTGSGANAVTVALERPDAFYRASD1SPPALETARKNAADLGARVEFAYGSWF
DTDMPSEGRWDLIYSNPPYIENCDKHLSQGDIRFEPQ1ALTDFSDGLSCIRTLAGGAP
DRIABGGFLLLEHGFDQGAAVRGVLABNGFSGVFTLPDLAGLDRYTLGKYMKHLK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="NWA0369, hemK, HemK protein, len: 273 aa; similar too e.g. HEMK_ECOLI 97186 HEMK protein (277 aa), fasta scores; E(): 0, 42.3% identity in 279 aa overlap. Contains PS00092 N-6 Adenine-specific DNA methylases signature"
                                                                                                                                                                                                                                                                                                                                                                                /translation="MQEQNRKSSFPIVMLLVSVALWIASLSNVAFYLGNHGSMEGLTV
LILGSIFASLDIRYCAVYANYVWLAAIVLLALRKKVVPVHAAFWGLALVAFSVKAVYV
DEAGNISDIVRYGAGFYLMYAAFAVASIGTFAGKNKERKAASAADGTKNDV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="NMA0370, probable integral membrane protein, len:
462 aa; similar to hypothetical proteins e.g. V325_HABIN
44440 hypothetical protein H10325 (450 aa), fasta scores;
E(): 0, 49.8% identity in 464 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGMPDSVRSGEGVVKWLLLSIILVWGMMSQNIIPIHIAFIPMIVPFLLLVFNRLKIDR
RLACVITGLUTTYMELPYOSGSGAIRDILACHIBSADGOLDVKNINWAAMAIPAL
GMLÄGLLLAEVYTYRERLYOSNNADTRANDAANRPOPSAYRSLAAVALAGVEAIOL
MYEDSLVLGAMLGFAVFWALGVINRDKANDVFGEGIKMMANVGFIMIAAQGFAAVNO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGHIOPLVESSMAIFGNSKGMAALAMLVVGLLVTMGIGSSFSTLPIIAAIYVPLCVGL
GFSPLATVAIVGTAGALGDAGSPASDSTLGPTMGLNADGQHDHIRDSVIPTFIHYNIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DAAGQVSQAGIIPVFNKGLEGGAKIALSYAMLGAFAMAITHSGLPQQLAGAVVRKLNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MNAVVVAVIVMLVLSLSRVHVVLSLTIGAFVGGAVAGMPLQNIA
                                                                                                            /note="NWA0368, probable integral membrane protein, len:
153 aa; contains four probable transmembrane domains"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="PS00092 N-6 Adenine-specific DNA methylases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /transl_table=11
/product="putative_integral membrane protein"
                                                                                                                                                                                                                                                                /product="putative integral membrane protein"
/protein_id="CABB3669.1"
/db_xref="GI:7379121"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(1279. .1288)
/note="Core DNA uptake sequence: gccgtctgaa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Core DNA uptake sequence: gccgtctgaa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Core DNA uptake sequence: gccgtctgaa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="CAB83671.1"
/db_xref="G1:7379123"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1578. .2966
/gene="NMA0370"
    'gene="NMA0368"
                                                                        /gene="NMA0368"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="hemK"
671. 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             831. .840
/gene="hemK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1162. .1171
/gene="hemK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLIAGWIAAMVL'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="hemK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2967. .3191
/gene="slyx"
2967. .3191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="hemK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . .1568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label=DUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  label=DUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  label=DUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RBS
gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
```

```
ထ
                                                               DEFINITION
                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
REFERENCE
AUTHORS
       RESULT
AC008323
                                                                                                                        ACCESSION
                                                                                                                                          VERSION
KEYWORDS
                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMMENT
                                                                                                                                                                               SOURCE
                                                   /traislation="MRHLRYIYSIYGNERKIMOLHILNNPKDAALAADAEFIKQSLFN
LLHEEASPLVVETVKLLSTSDDSAALIEKVLPQLDEQQTHDLTLACGLFAQILNIAED
VHERRRQIHEEAGRGGAEGSLTETYRRLKAGKADGKSVQRQLDNTSYTAVLTAHPTE
VQRQTVLNFNRIRALLPQREKCTHADALARLRREIDTILLGLMQTSSTRRHKLSVND
BINNGYSIFPRASFLPRLYKKMEHDPQTAYDDYRYPDILKIGGWIGGDRDGNPFVS
AETLRFAFRRHADAVFFFYRGELDKLYRELDSIRRVKVNGPYMALSDKSPDETARA
BEDYRRAIAVIMARAMGKARALGLGMGCKFGFLEPYASAQGFLDDLKKLQHSLIDNGS
                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA HTG 03-JAN-2000
*** SEQUENCING IN PROGRESS ***, in ordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                          DD 106727 GCATCTTAAACAAAAAACGCAAAAAGCCATGATGATGACGAAAGCGAGTTTATCCGCGCG 106668
                                                                                                                                                                                                                                                                                                                                                                                               Db 106667 AGCGAAGCATTATTTGAACACATCGAAGACCAAATCGACGAAAACGCCTGGGATTTCGAC 106608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49999 TIGGCCATGATCTGGGGGTCCCATTAGCCACAAAAGGTGTAGGCCGAAAATGCTCTCAGC 50058
                                                                                                                                                                                                                                                                                                                                                           248 cgtaaaccggtaacgcatcacctgacggaagaaatgcaaaaagggtttcattacaccatt 307
                                                                                                                                                                                                                                                                                  188 gaataacatatgaaatggttggaagaatccattatggccaaacgcggtgttggtgccggg 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ttgatcaagaactggcagctttcctggccacgaatggagaatgccgaaaatattatgagt 985
                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rockville, MD, USA

This sequence was identified as CDM:10211861 by the submitter. For more information on this record e-mail to fly@celera.com. * NOTE: This sequence will be replaced

* Dt the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adams, M. and Venter, J.C.
Direct Submission
Submitted (30-DEC-1999) Celera Genomics, 45 West Gude Drive,
                                                                                                                                                                                                                                                      .,
                                                                                                                                                                                                               DB 2; Length 349061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 39.6; DB 43; Length 92918;
Pred. No. 4.2;
0; Mismatches 39; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="phosphoenolpyruvate carboxylase"
/protein_id="CAB83675.1"
/db_xref="GI:7379127"
                                                                                                                                                                                                                                                78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
20547 c 20610 g 26042 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39;
                                                                                                                                                                                         2.9%; Score 41.2; DF
                                                                                                                                                                                                                             Pred. No. 1.8;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC020050.1 GI:6664847
HTG; HTGS_PHASE2.
fruit fly.
Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.7%;
61.8%;
                                                                                                                                                                                                                             53.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92918 bp
                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .92918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 2.77
Best Local Similarity 61.8
Matches 63; Conservative
                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25719 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC020050
                                                                                                                                                                                                                                            88;
                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC020050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /ERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
```

·.

```
AL Submitted (02-Augusty, T., Mann, Melubuly, T., Zhang, K., Zheran, L.L., and Rubin, G.M.

Direct Submission

AL Submitted (02-Aug-1999) Drosophila Genome Center, Lawrence Berkeley Laboratory, MS 64-121, Berkeley, CA 94720, USA

On Feb 11, 2000 this Sequence version replaced gi:5670417.

For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu. All contigs in this submission meet the following cutoffs: length >= 200 bases.

* NOTE: This is a 'working draft' sequence record is consists of 92 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as true order of N. but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as as as as as as a true available and the accession number will
         AC008323 123296 bp DNA HTG 10-FEB-2000 Drosophila melanogaster chromosome 2 clone BACR03G07 (D850) RPCI-98 03.6.7 map 24D-24D strain y; cn bw sp, *** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            " (bases 1 to 123296)
Celniker.S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G.,
Butenhoff.C., Champe,M., Chavez,C., Chew,M., Cieseiolka,L.,
Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L.,
Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L.,
Kin,E., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Mazda,P.,
Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S.,
Pfeiffer,B., Poon,L., Sequeira,A., Sethl,H., Snir,E.,
n.t., Squeira,A., Sethl,H., Snir,E.,
                                                                                                                                                                                                                                                                                                                                                                           l (Dacker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Hobole, C., Champe, M., Galle, R., George, R.A., Harris, N.L., Hinkle, A., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Lee, B., Lewis, S., Li, P., Ling, H., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., R.Chards, S., Sethi, H., Svirskas, R.R., Wan, K.H., Webster, D., Sequencing of Drosophila melanogaster
                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pteryyota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contig of 840 bp in length gap of unknown length is contig of 1246 bp in length contig of 738 bp in length gap of unknown length gap of unknown length contig of 697 bp in length gap of unknown length contig of 648 bp in length gap of unknown length contig of 574 bp in length gap of unknown length gap of unknown length gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of 1030 bp in length
unknown length
of 1122 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of 655 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of 938 bp in length
unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       contig
gap of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            contig c
                                                                                            92 unordered pieces.
                                                                                                                                                                                                                                         Drosophila melanogaster
                                                                                                                                                   AC008323.2 GI:6957898
123296 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3761:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4489:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5143:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5958:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8006:
                                                                                                                                                                                  HTG; HTGS_PHASE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        be preserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              921
22167
22985
330655
33762
33762
44540
4550
55224
55879
6977
8087
                                                                                                                                                                                                              fruit fly.
                                                                                                                    AC008323
```

```
unknown length
of 584 bp in length
funknown length
in 684 bp in length
funknown length
funknown length
g of 869 bp in length
g of 189 bp in length
if unknown length
g of 1199 bp in length
g of 1199 bp in length
g of 1185 bp in length
g of 1185 bp in length
g of 1185 bp in length
g of 123 bp in length
g of 123 bp in length
g of 123 bp in length
g of 125 bp in length
g of 1172 bp in length
g of 1175 bp in length
g unknown length
g of 855 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            f unknown length
g of 1774 bp in length
f unknown length
g of 1603 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              f unknown length
g of 1084 bp in length
f unknown length
of 950 bp in length
f unknown length
g of 1529 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          f unknown lengtn
g of 1859 bp in length
inknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    i or ...
E unknown lengtn
g of 1032 bp in length
f unknown length
g of 846 bp in length
f unknown length
g of 755 bp in length
f unknown length
g of 1194 bp in length
f unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bp in length
length
bp in length
                                                                                                                   d of 585 by in length f unknown length g of 468 by in length f unknown length g of 819 bp in length f unknown length g of 757 bp in length f unknown length g of 668 bp in length f unknown length f unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bp in length
length
                                                                                                                                                                                                                                                                                                                                     of 1018 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              length
                     gap of contig gap of contig gap of gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gap of
contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contig
gap of
gap of
contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                   contig
gap of
contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contig
gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gap of
contig
                                                                                                                                               gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gap of
                                                                                                                                                                                      gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gap of
                                                                                                                                                                                                                                                                                                                                                                                                    gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52571:
52651:
                                                            1049:
                                                                                                                                                                                                       113537
1144356
1151938
1151938
1151938
1151938
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
1171039
                     10135
10215
10970
11050
12244
12324
12909
12909
```

k 2776 bp in length known length in length 18734 bp in length known length left 6620 bp in length known length bp in length length bp in length length of 5255 bp in length unknown length of 633 bp in length unknown length length bp in length length bp in length length bp in length bp in length length bp in length length unknown lengrn y of 710 bp in length bp in length length length bp in length length bp in length bp in length bp in length bp in length length bp in length bp in length bp in length of 699 bp in length of 641 bp in length unknown length length length length length length length length unknown of 1677 1719 contig gap of contig gap of gap of contig gap of gap of contig gap of gap of contig gap of gap of gap of 110847: 71812 552652 553813 553813 55384 557319 577399 577399 60070 60150 60150 60150 60150 64170 107136 107216 107849 107929 108628 108708 109418 109498 110047 110127 110768 75481 75561 77831 77911 80073 80153 81872 81952 83956 84036 86170 01801 73804

Query Match 2.7%; Score 39.6; DB 51; Length 123296; Best Local Similarity 61.8%; Pred. No. 4.4; Matches 63; Conservative 0; Mismatches 39; Indels 0; Gaps

ö

RESULT

```
f unknown length
g of 1291 bp in length
f unknown length
g of 1217 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              f unknown length
g of 1806 bp in length
f unknown length
g of 1498 bp in length
                                                                                       unknown length
of 1005 bp in length
                                                                                                                                                                                                                                          of 929 bp in length
unknown length
of 1221 bp in length
                                                                                                                                                                                                                                                                            unknown length
of 1272 bp in length
                                                                                                                                                                                                              length
                                                                                                                                                                                                                                                                                                                                   unknown length
of 1259 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown length
of 1396 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown length
of 2180 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown length
of 1754 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown length
of 1656 bp in length
                                                                                                                                                           length
                                                                                                                                                                                                                                                                                                                                                                              in length
                                                                                                                                                                                                                                                                                                                                                                                                       in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown length
of 1602 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lengtn
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of 1554 bp in length
unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1874 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown length
of 2038 bp in length
unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bp in length
                                               of 918 bp in length
                                                                        of 804 bp in length
                                                                                                                                                                                     of 824 bp in length
                                                                                                                                                                                                                                                                                                                        781 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      935 bp in length
                                                                                                                                             length
                                  unknown length
                                                              length
                                                                                                                     length
                                                                                                                                                                        Length
                                                                                                                                                                                                                             unknown length
                                                                                                                                                                                                                                                                                                           unknown length
                                                                                                                                                                                                                                                                                                                                                                unknown length
                                                                                                                                                                                                                                                                                                                                                                                           unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown length
of 1834 bp in 1
                                                                                                                                                                                                    length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown length
of 1869 bp in 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown length
                                                                                                                                                                                             unknown length
of 1271 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              length
                                                                                                                                                        of 1117 bp in
unknown length
                                                                                                                               1330 bp in
                                                                                                                                                                                                                                                                                                                                                                                                       of 1507 bp
                                                                                                                                                                                                                                                                                                                                                                             of 1015 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown 1
of 1577 k
unknown 1
of 1055 k
unknown 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown of 2485 k
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
of 1519 h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
of 2432 l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of
                                                                                                                                 oţ
                                                                                                                                                                                                                                                                                                                         οį
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 οĮ
                                             contig
gap of
contig
gap of
contig
gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gap of contig
       gap of
contig
gap of
                                                                                                                                                        contig
gap of
contig
gap of
                                                                                                                                                                                                                                        contig
gap of
contig
gap of
contig
gap of
contig
gap of
                                                                                                                                                                                                                                                                                                                                                             gap of contig gap of contig gap of contig gap of contig gap of contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gap of contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contig
gap of
                                                                                                                                                                                                              contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gap of contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contiq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of
                                                                          12931:
                                                                                                                                                                                                                                                        .9967:
                                                                                                                                                                                                                                                                   1188:
                                                                                                                                                                                                                                                                                                           2620:
                                                                                                                                                                                                                                                                                                                                                                                           5915:
                                                                                                                                                                                                                                                                                                                                                                                                                                              8873:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1566:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64898:
64978:
                                                                                                                  14096:
                                                                                                                                                                                                                8878:
                                                                                                                                                                                                                             8958:
                                                                                                     14016:
                                                             2127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54811
                 9858
11050
11130
12128
12128
13012
14017
14097
15624
115507
115507
115508
117508
                                                                                                                                                                                                                                       18959
119888
119688
11968
21189
22541
22561
23402
23482
24741
25836
25936
27423
27503
227503
28794
30091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30171
31567
318647
338647
338907
35661
36676
38412
38412
38412
38412
38412
38412
38412
38412
38412
38412
38412
38412
38412
38412
38412
38412
38412
38412
38412
38412
38412
38412
38412
38412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48344
50568
50648
53133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53213
54732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54812
56681
56761
58315
58335
58395
60269
60349
62781
62861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission

AL Submission

Submitted (28-APR-1999) Drosophila Genome Center, Lawrence Berkeley
Laboratory, MS 64-121, Berkeley, CA 94720, USA

On Aug 2, 1999 this sequence version replaced gi:5649319.

For further information about this sequence, including its location
and relationship to other sequences, please visit our sequence
archive Web site (http://www.fruitfly.org/sequence/) or send email
to bdgp@fruitfly.berkeley.edu. All contigs in this submission meet
the following cutoffs: length >= 200 bases.

* NOTE: This is a 'working draft' sequence. It currently
consists of 83 contigs. The true order of the pieces

* is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as

* Tuns of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                      SM Drosophila melanogaster
Eukaryota: Metazoa; Arthropoda: Tracheata; Hexapoda; Insecta;
Eukaryota: Metazoa; Arthropoda: Tracheata; Hexapoda; Insecta;
Pterygota: Neoptera: Endopterygota; Diptera; Brachycera;
Muscomorpha: Ephydroidea; Drosophilae; Drosophila

I (bases 1 to 13083)
S (Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G.,
Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L.,
Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L.,
Hoskins, R.A., Houstsofn, R.A., Hummasti, S.R., Karra K., Kearney, L.,
Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P.,
Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S.,
Pfaiffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E.,
Rubin, G.M.
            AC007420 130583 bp DNA HTG 20-SEP-1999
Drosophila melanogaster chromosome 2 clone BACR07M10 (D630) RPCI-98
07.M.10 map 24A-24D strain y; cn bw sp, *** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                                                                                         2" (bases 1 to 130583)
Celniker,S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G.,
Butenhoff,C., Champe,M., Chavez,C., Chew,M., Clesiolka,L.,
Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L.,
Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L.,
Kim,E., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Mazda,P.,
Moshrefi,A.R., Moshrefi,M., Nixon, Facleb,J.M., Park,S.,
Pfeiffer,B., Poon,L., Sequeira,A., Sethi,H., Snir,E.,
Pyliskas,R.R., Wan,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              f unknown length
g of 582 bp in length
f unknown length
g of 1219 bp in length
f unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown lengtu
y of 578 bp in length
whitenown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of 893 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             808 bp in length known length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of 906 bp in length
unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown length
of 898 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of 782 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of 706 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       680 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of 925 bp in length
unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown length
                                                                                                                                                                                                                                                                                                               Sequencing of Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               σĘ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contig
gap of
contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contig
gap of
contig
gap of
contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gap of
                                                         83 unordered pieces.
                                                       ***, 83 unordered piece
AC007420
AC007420.3 GI:5670587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2743: 2823: 3716: 3796: 4604: 4684: 5390: 5470:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6048:
6128:
7034:
7114:
7794:
                                                                                               HTG; HTGS_PHASE1
                                                                                                                                                                                                                                                                                                                                 Jnpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                783
863
11525
22744
22824
33717
33717
3717
55491
6049
61049
61049
7013
7115
77795
88800
                                                                                                            fruit fly
                                                                              VERSION
KEYWORDS
SOURCE
ORGANISM
                         DEFINITION
                                                                                                                                                                                                                                                                                                                 TITLE
JOURNAL
RÉFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
JOURNAL
                                                                    ACCESSION
                                                                                                                                                                               REFERENCE
                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                         AUTHORS
AC007420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMMENT
```

```
ENARTOCAS MENEZORS AFILTROGAS, TEACHRAIDS
ENARTOCAS MENEZORS AFILTROGAS, TEACHRAIDS
BLOGGER, TO 304383)

Adams, M.D., Celniker, S.E., Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Scherer, S.E., Li, P.W., Hoskins, R.A., Galle, R.F., George, R.A., Lewis, S.E., El, P.W., Mang, C.M., Menderson, S.N., Sutton, G.G., Wortman, J.R., Yandell, M.D., Zhang, O., Chen, L.X., Randon, R.C., Rogers, Y.H., Blazel, R.G., Change, M., Pfeiffer, B.D., Man, G.G., Abrill, J.F., Aphayani, A.A., H.J., Basu, A., Brandon, R.C., Bayraktaroglul, B. Beasley, E.M., Besson, K.Y., Bancos, P.V., Berman, B.P., Bhandari, D., Ballew, R.M., Basu, A., Bayraktaroglul, B. Bosslay, E.M., Bencos, P.V., Berman, B.P., Bhandari, D., Bolshakov, S., Borkova, D., Bochcham, R.P., Bouck, J., Broxtseid, P., Brother, J., Bolthakov, S., Borkova, D., Bochcham, R.P., Bolcher, A., Cadde, E., Carter, A., Chandra, I., Bund, S., Bolthakov, S., Borkova, D., Bochcham, R., Bolcher, A., Dend, E., Carter, A., Chandra, I., Delcher, A., Eutler, F., Loudey, S., Dahlke, C., Davenport, L.B., Davies, P., de Pablos, B., Delcher, A., Eutler, F., Evaley, S., Dahlke, C., Davenport, L.B., Davies, P., de Basch, M., Posler, C., Gabriellan, A.E., Garg, N.S., Guan, P., Hermandez, J.R., Houck, J., Hostin, D., Houm, P., Durbin, M. Fosler, C., Gabriellan, A.E., Garg, N.S., Galsser, K., Houck, J., Hostin, D., House, C., Davender, G., Marris, M., Merris, N. L., Harris, N. Marris, M. Merkle, B., Morlander, J. M., Hold, J., Li, Z., Liang, T., Lill, M., Moshrefil, A., Moshrefil, A., Moshrefil, M., Merkle, B., Morlander, J. M., Moshrefil, M., Merkle, B., Morlander, J. M., Pollard, J., Moshrefil, M., Merksenhan, P., Sandel, P., Scheeler, F., Shen, H., Shue, B., Spending, Sanders, R.D., Moshrefil, M., Moshrefil, M., Mang, S., Yan, Wootage, T., Gabor, M., Weinschon, W., Stupaki, M., Wang, S., Moy, M., Worter, E., Wang, S., Land, M., Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 304383)
Adams, M.D., Celniker, S.E., Gibbs, R.A., Rubin, G.M. and Venter, C.J.
Direct Submission
                                                                                        Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WD, USA
Location/Qualifiers
1. 304383
//Organisma* Drosophila melanogaster*
//db_xref="taxon:7227"
//chromosome="2L"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="CG15419"
/product="CT35478"
/db_xref="FLYBASE:FBan0015419"
/db_xref="FLYBASE:FBqn0040710"
/evidence=not_experimental
complement(<9367. >9540)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="CG15419"
/db_xref="FLYBASE:FBan0015419"
/db_xref="FLYBASE:FBgn0040710"
/db_dedence=not_experimental
complement(9367. 9540)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(<9367. .>9540)
     of 16, complete sequence.
                                        AE003579.1 GI:7295765
                        AE002638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rockville,
                    ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
                                                                                                                                                             REFERENCE
                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCUS AE003579 304383 bp DNA INV 22-MAR-2000
DEFINITION Drosophila melanogaster genomic scaffold 142000013386046 section 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     926 ttgatcaagaactggcagctttcctggccacgaatggagaatgccgaaaatattatgagt 985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 39.6; DB 41; Length 130583; Pred. No. 4.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  of 10767 bp in length
                                                       length
bp in length
                                                                                      length
bp in length
                                                                                                                                                                                                                                                                                                      unknown length
of 2687 bp in length
                                                                                                                                                                                                                                                                                                                                           unknown length
of 4033 bp in length
                                                                                                                                                                                                                                                                                                                                                                              unknown length
of 2973 bp in length
                                                                                                                                            in length
                                                                                                                                                                               bp in length
                                                                                                                                                                                                                  bp in length
                                                                                                                                                                                                                                                    bp in length
                                                                                                                                                                                                                                                                    length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of 888 bp in length
unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of 646 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of 727 bp in length
unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of 720 bp in length
unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of 659 bp in length
unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of 689 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of 581 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     901 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of 562 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of 650 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of 718 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of 672 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of 684 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of 643 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93438 ATCGGGCATCAAGTTCGCTGCAGGATGCGCGGAGGAGA 93479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       986 attggcagtgcacgtccgctggaggatgcgacgcgaattgca 1027
                                                                                                                                                                                              length
                                                                                                                                                                                                                                   length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown length
                                                                                                                           ength.
                                                                                                                                                             length
                                                                                                                                                                                                                                                                                                                                                                                                                   unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of 772 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unknown
                                                                                                                                              of 3132 l
unknown
                                                                                                                                                                                                                                                      of 2616
                                                                                                                                                                                                                                                                                       of 5028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                          of 2711
                                                                                                                             unknown
                                                                                                                                                                                                                                 unknown
                                                                                                                                                                                                                                                                      unknown
                                                                                                                                                                                                  unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ō
                                                                                                                                                                                                                                                                                                                        contig
gap of
contig
gap of
                                   contig
gap of
contig
gap of
contig
                                                                                                                                                                             contig
gap of
contig
gap of
                                                                                                                                                                                                                                                                    gap of
contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                 gap of contig gap of contig gap of contig gap of gap of gap of gap of gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               contig
gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gap of
contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                              contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gap of
                                                                                                                                          contig
                                                                                                                                                                                                                                                    contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gap of
                                                                                                                                                             gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.7%;
61.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124188:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121368:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115870:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118949:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20490:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21288:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22120:
                                                                                                                                                                                                                                                                                       91696:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114990:
                                                                                                                                                                                                                                                                                                                                                                                              101629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity 61.8
Matches 63; Conservative
64979
66964
67044
69575
69655
72366
72446
75170
78382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16610
17498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118870
118950
119639
119719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121289
                                                                                                                                                                                                                                                  83973
86589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114991
115071
115791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120491
120571
                                                                                                                                                                                                                                                                                                                                           94464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
AE003579/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         õ
```

ò

mRNA

gene

CDS

```
/do.xref="FLYBASE: FBan0002818"
/db_xref="FLYBASE: FBgn0031566"
/db_xref="FLYBASE: FBgn0031566"
/db_xref="TLYBASE: FBgn0031566"
/db_xref="G1: 7295769"
.db xref="G1: 7295769"
.db xref=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="FLYBASE:FBan0010030"
/db_xref="FLYBASE:FBq003156".2649,25705. .26284,
26341. .26533,26636. .26752,26809. .26911,26971. .27072,
27311. .27408,27720. .27895,27955. .28088,28151. .28871,
2807. .28870.2945. .29464,30470. .30624,30795. .30916,
31389. .31506,31753. .31967)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .26284,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSLEQUKKLKVYHIAEGLSRETRSFHNDCLEHQPPQLCDVLDALDVHVGFNIEIKW
SQRLEDGKMEEEEHVVDRULYIDCLEDVILKRAGNRRIVLSCFDPDICTILKKQNR
YPVMFLTLGRFTKVQKYMDPRGNSMELAVHHAAGNRRIVLSCFDPDICTILKRQNR
YPVMFLTLGRFTKVQKYMDPRGNSMELAVHHAVAMEFLGVVAHTEDLLRDPSQVNLAK
ERGLVLECWGDDDNRSOTIKLLKELGLHAIIYDKMOVLTTREVKQSYFHLQAKDSQVRE
LILKLQALEDMHVWHTSADGNBEDQA
join (23524 . 23991, 24270 . 24433, 24726 . 25649, 25705 . 2628
26341 . 26533, 26636 . 266752, 26809 . 26911, 26971 . 27072,
27211 . 27408, 27720 . 27895, 27955 . 28088, 28151 . 28371,
28807 . 238070, 292464, 30470 . 30624, 30795 . 30916,
//gene="CGL00030"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SAEGKITTRKLSRSIPPYPHAVRVKNGIRVYEYSEPRKQSYKSSLWKBAYNVSRNRRT
HAGHFTCFISDIPPAVGYCRANRSKGIPVIKREREMCSRLLIIDNDFDFEIRNAKNTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRI HFHFGGLSLSVNKVEEEETRKDFIKLFVGRSFETSMDQYPDENEEFELQYQDELE
LLEDLPDEFNAYDGPSTSKQAAEKQKENRAPVAALRDSTRLGNSTLGSPQLSQITFGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MEGDKVVFHSSDLPYEYLYDDEKHVSHMPDSKLSVRNILDSAYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
complement(join(19878. .19997,20083. .20229,20282. .21739,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HS288L1 118593 bp DNA PRI 12-DEC-1999
Human DNA sequence from clone RP1-288Ll on chromosome 22 Contains an STSs, GSSs and genomic marker D22S1152, complete sequence. 282196
282196.2 GI:6572205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DD 140969 TIGGCCATGATCTGGGGGTCCCATTAGCCAAAAAGGGTGTAGGCCGAAAATGCTCTCAGC 140910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       926 ttgatcaagaactggcagctttcctggccacgaatggagaatgccgaaaatattatgagt 985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.7%; Score 39.6; DB 34; Length 304383; 61.8%; Pred. No. 5.2; tive 0; Mismatches 39; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qy 986 attggcagtgcacgtccgctggaggatgcgacgcgaattgca 1027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="CG10030 gene product"
/codon_start=1
/db_xref="FLYBASE:FBan0010030"
/db_xref="FLYBASE:FBan0031565"
/protein_id="AAF51072.1"
/db_xref="G1:7295770"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="CT28231"
/db_xref="FLYBASE:PBan0010030"
/db_xref="FLYBASE:FBgn0031565"
<23524. .>31967
                                                                                                                 /note="CG2818 gene
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="CG10030"
                                        21895. .22293))
/gene="CG2818"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="CG10030"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
HS288L1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
            CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                                                                                complement(join(<10708. .10730,12622. .12750,13130. .13733,
13815. .14033,14369. .14563,14624. .14741,14797. .>15005))
/gene="Shaw"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="FLYBASE:FBan0002822"
/db_xref="FLYBASE:FBan0003386"
/db_xref="FLYBASE:FBan0003386"
/db_xref="G1:J295767"
/tb_xref="G1:J295767"
/tb_xref="MNLINMDSENRYVLNVGGIRHETYKATLKKIPATRLSRLTEALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FLDKTOTNALIAFFYIECCONAWFTFEILVRFISSPRIWEFTKSSVNIIDYTATLSFY
IDLVLORFRASHLENADILEFFSIIRIMRLFKLTRHSSGLKTLIQTFRASAKELTLLVF
FLVLGIVIRASLYYYAERIOPNPHNIPNSIELGENWALVTMTVGYGDNAPKTYIGMF
VGALCALAGVLTIALPVPVIVSNFAMYYSHTQARAKLPKKRRVLPVEOPROPRLPGA
PGGYSGCGTGEGGGPHGGPMGSGGTGPRRMNNTKDLVSPKSDMAFSFD"
<18658. .>19506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VMEYVATHQDKWNTCTEILANBARKDQIQLNIQLDALKADVSNIKASQLSKDEKLDRM
EEROFAMHESLETINRYLIVKLIDRTKLQLEAIKTMDYMKAGMOSYESAINGVOCLQP
GFERICBRYRYTIEEDYPELMNIDAQAKCRMGGHLASIKTKQBEDAIVEKLDDSKSYFL
GVNEWTKGDRYSASGKSCLYHEWGPGEPHNNNDQERCVSILRKLMHVGNCTYERRF
                                                                                                                                                                                                                                                                               /translation="MTASGIGTTSATGATSAPQPATPLPSIAVSTTASVGKDLGISTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NYDPTLNEYFFDRHGVFAQVLNYYRTGKLHYPTDVCGPLFEEELEFWGLDSNQVEPC
CWMTYTQHRDTQETLAVLDRLDLDTEKPSEEELARKFGFEEDYYKGTISWWQEMKPRI
WSLFDEPYSSNAAKTIGVVSVFFICISILSFCLKTHPDMRVPIVRNITVKTANGSNGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MFRLSVLVLNLLLVSHEFSAGTAKIEIQPLPALCNGYCFPTLKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21895. .22294,22650. .>22974))
/gene="CG2818"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="rLYBASE:FBan0002822"
/db_xref="FLYBASE:FBgn0003386"
complement(join(10708. .10730,12622. .12750,13130. .13733,
13815. .14033,14369. .14563,14624. .14741,14797. .15005))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="FLYBASE:PBan0003410"
/db_xref="FLYBASE:FBgn0031567"
/protein_id="AAF51070.1"
/db_xref="G1:7295768"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="FLYBASE:FBan0003410"
/db_xref="FLYBASE:FBgn0031567"
18658. .19506
//gene="CG3410"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="CT9622"
/db_xxef="FLYBASE:PBan0002822"
/db_xxef="FLYBASE:FBgn0003386"
complement(<10708. .>15005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="CT11463"
/db_xref="FLYBASE:FBan0003410"
/db_xref="FLYBASE:FBgn0031567"
<18658. >19506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="FLYBASE:PBan0002818"
/db_xref="FLYBASE:PBqn0031566"
complement(<19878. .>22974)
/gene="CG2818"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="FLYBASE:FBan0002818"
/db_xref="FLYBASE:FBgn0031566"
                                                                                                                         /db_xref="FLYBASE:FBan0015419"
/db_xref="FLYBASE:FBgn0040710"
                                                /note="CG15419 gene product"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="CG3410 gene product"/codon_start=1
                                                                                                                                                                                                      /evidence=not_experimental
/protein_id="AAF51068.1"
/db_xref="G1:7295766"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Shaw gene product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="CT9610"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="Shaw"
/note="CG2822"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /map="24B-24C"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="CG3410"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="CG3410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="Shaw"
```

gene

CDS

mRNA

gene

mRNA

```
/note="MIR repeat: matches 23. .121 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                          repeat_region
                                                                                                                 repeat_region
                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                   together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWHSSPROT; Tr., TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 22, constructed by the Sanger Centre Chromosome 22 Mapping Group. Further information can be found at
                                                                                                                                                                                         Direct Submission
Submitted (08-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Dec 13, 1999 this sequence version replaced gi:1903194.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Roswell
or further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1325. 4939
'note="HERV16 repeat: matches 1665. .2289 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4975. .5684
/nocte="RERV16 repeat: matches 2344. .3072 of consensus"
5924. .6339
/nocte="HERVL repeat: matches 3442. .3860 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142. .852
/note="L1PA8 repeat: matches 5434. .6163 of consensus"
853. .1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2248. .2413
/note="HERVL repeat: matches 3359. .3525 of consensus"
3173. .373 repeat: matches 8. .223 of consensus"
/note="LTR33 repeat: matches 8. .223 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6296. .6578
/note="match: STS: Em:F08316"
6452. .6566
/note="HERVL repeat: matches 4031. .4115 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (037. .1809
'note="HERVL repeat: matches 3871. .4641 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5825. ,7958
/note="HERVL repeat: matches 4115. ,5247 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3673. .4275
/note="LIM4 repeat: matches 2681. .3306 of consensus"
4325. .4939
                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5337. .6824
/note="AluSc repeat: matches 13. .299 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="MSTA repeat: matches 185. .314 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.sanger.ac.uk/HGP/Chr22
http://www.sanger.ac.uk/HGP/Chr22
http://www.sanger.ac.uk/HGP/Chr22
http://www.sanger.ac.uk/HGP/Chr22
hark Cancer Institute by the group of Pieter de Jong. For Jetals see http://bacpac.med.buffalo.edu/
VECTOR: pcrPAC2://bacpac.med.buffalo.edu/
This sequence is the entire insert of clone RPI-288LI.
Location/Qualifiers
1. 118593
/docama-"Homo sapiens"
/docama-"Homo sapiens"
/chromosome-"22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="MSTA repeat: matches 1. .200 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="RP1-288L1"
/clone_lib="RPCI-1"
                                                                                                        Eutheria; Primates; Ca
1 (bases 1 to 118593)
HTG; D22S1152.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  feature key.
                                                                                                                                                                  Burton, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
                                                    ORGANISM
                                                                                                                                                               AUTHORS
TITLE
                                                                                                                                     REFERENCE
                                                                                                                                                                                                                         JOURNAL
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                          COMMENT
```

```
/note="AluSx repeat: matches 1. 310 of consensus"
20064. .20128
20064. .20128
20456. .20899
20456. .20899
20456. .20899
20456. .20899
21834. .23162
21834. .23162
23163. .23463
23163. .23463
23163. .23463
23464. .23735
                                                                         /note="L2 repeat: matches 2624. .2748 of consensus" 9068. .9178
/note="MEM94 repeat: matches 1. .113 of consensus" 9957. .15197
/note="L1PA2 repeat: matches 900. .6146 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               // Anote="MIR repeat: matches 90. .231 of consensus" 29619. .29735 // Anote="L2 repeat: matches 2418. .2529 of consensus" 31018. .31154 // Anote="L2 repeat: matches 2240. .2400 of consensus" 31217. .31587
                                                                                                                                                                                                                                                                                   /evidence-not_experimental
17316. .17875
//note-"SVA repeat: matches 798. .1363 of consensus"
complement(17752. .18176)
/note-"match: GSS: Em:AQ113498"
17896. .18316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .2749 of consensus"
                                                                                                                                                                     15193. 15979
/note="L1PA2 repeat: matches 1. .776 of consensus"
16282. .17315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31217. .31587
/note="THBIC repeat: matches 1. .371 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="AluSg repeat: matches 1. .264 of consensus"
28220. .28347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .256 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                         .262 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .173 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .152 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .261 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .262 of consensus"
                                                                                                                                                                                                                               .955 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .251 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .2707 of
...c="11 copies 2 mer aa 100 conserved"
8803. .8918
/note="L2 repeat: match"
9068. .917p
                                                                                                                                                                                                                         /note="SVA repeat: matches 14.
16843. .17747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="L2 repeat: matches 2630.
18682. .18805
                                                                                                                                                                                                                                                                                                                                                                                              /note="match: GSS: Em:AQ802108"
18158. .18396
/note="MIR repeat: matches 15.
18529. .18648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="MIR repeat: matches 18.
28620. .28790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="MIR repeat: matches 52.
19153. .19462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="MIR repeat: matches 89. 28835. .28983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="MIR repeat: matches 47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="MIR repeat: matches 28. 33524. .33626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31723. .31850
/note="L2 repeat: matches
                                                                                                                                                                                                                                                                  /note="CpG island"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12433
```

GI:7227234

AE002546.1

```
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                     TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                             Jabola. Autuoud.

Judga. "MERTOR repeat: matches 136. .593 of consensus"
40083. .40294
Anote="MERTOR repeat: matches 49. .261 of consensus"
Anote="Li repeat: matches 2616. .2749 of consensus"
Anote="Li repeat: matches 2592. .2673 of consensus"
Anote="Li repeat: matches 2592. .2673 of consensus"
Anote="MIR repeat: matches 48. .145 of consensus"
Anote="MERA1B repeat: matches 1. .634 of consensus"
A2285. .48322
Anote="MIRTIG repeat: matches 2. .512 of consensus"
A3464. .44153
Anote="MIRTIG repeat: matches 4683. .5399 of consensus"
A3464. .44153
Anote="MIRTIG repeat: matches 4683. .5399 of consensus"
A3464. .44153
Anote="mirtig 6585 Em: A4489)
Anote="mirtig 6585 Em: A4489]
Complement(44254. .44730.
Anote="mirtig 6585 Em: Anithmatches 4683. .5399 of consensus"
Anote="mirtig 6585 Em: Anithmatches 44789]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94608 TATTACCAACCTCATAAGCAGGCTGGGGTGCTGCCAGTTAATACATCACCTGGATATGCA 94549
                                                                                                                                                  35.234. 35.231

35.234. 35.296

75.234. 35.296

70.05e="L2 repeat: matches 2647. .2709 of consensus"
35.55. 38.6499

70.05e="MIRGO repeat: matches 2000. .2510 of consensus"
36.499. .37292

70.05e="MIRGO repeat: matches 1. .801 of consensus"
37.832

70.06="MIRGO repeat: matches 9. .294 of consensus"
37.832

70.06="A.37967"

86.71. .38783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                160 tgtaactaaacgctataaattacgtggagaataacatatgaaatggttggaagaatccat 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        220 tatggccaaacgcggtgttggtgccgggcgtaaaccggtaacgcatcacctgacggaaga 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94548 TTAGCAAAAGGTCTTCCTCCCAAGTGGACACACACCTCCACACTGCACTCATGAT 94492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="L2 repeat: matches 2293. .2749 of consensus"
45279. .45426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              280 aatgcaaaaagagtttcattacaccattggcccttattccacacccgtcctgaccat 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 //note="MIR repeat: matches 87. .243 of consensus" 47053. .47490 /note="MILTIC repeat: matches 1. .465 of consensus" 48174. .48418 repeat" 48187. .48488
                                                                 /note="L2 repeat: matches 2576. .2646 of consensus"
34305. .34649
                                                                                                                                                                                                                                                                                                                                                                            .145 of consensus"
                           .262 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 118593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                               note="Alusq repeat: matches 1. .309 of 35067. .35231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="match: GSS: Em:AQ790304"
14690. .44996
note="match: GSS: Em:AQ618052"
14839. .45277
      33957. .34137
/note="MIR repeat: matches 52.
34184. .34257
                                                                                                                                                                                                                                                                                                                                                                                 /note="MIR repeat: matches 22. 39632. .40082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 Match 2.7%; Score 39.4; Local Similarity 51.4%; Pred. No. 5; es 91; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44690.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44839.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
             repeat_region
                                                          repeat_region
                                                                                                   repeat_region
                                                                                                                                           repeat_region
                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QΩ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

AE002546 10619 bp DNA BCT 03-APR-2000 Neisseria meningitidis serogroup B strain MC58 section 188 of 206 of the complete genome. AE002546 AE002098

RESULT 12 AE002546 LOCUS DEFINITION

ACCESSION

```
Tettelin, H., Saunders, N.J., Heidelberg, J., Jeffries, A.C.,
Nelson, K.E., Eisen, J.A., Ketchum, K.A., Hood, D.W., Peden, J.E.,
Nelson, R.J., Nelson, W.C., Gwinn, M.L., DeBoy, R., Peterson, J.D.,
Hickey, E.K., Haft, D.H., Salzberg, S.L., White, O., Fleischmann, R.D.,
Dougherty, B.A., Mason, T., Ciecko, A., Parksey, D.S., Blair, E.,
Cittone, H., Clark, E.B., Cotton, M.D., Utterberk, T.R., Khouri, H.,
Qin, H., Vamathevan, J., Gill, J., Sarlato, V., Masignan, V.,
Pizza, M., Grandi, G., Sun, L., Smith, H.O., Fraser, C.M., Moxon, E.R.,
Rappuoli, R. and Venter, J.C.
Direct Submission

L. Submitted (17-MAR-2000) The Institute for Genomic Research, 971Z
Medical Center Dr. Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MSDSKTKERATFGTRRAFMIAAIGSAVGLGNIWRFPYIAFENGG
GAFILPYLVALLTAGIPLLLDYAIGHRYRGSAPLAFRRLGRWFEPVGWWNVMINIVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="witrplindryvkrleabertasgivlpgaaaekpDmgeVIavg
AGKIGKDGSRRPLDVKVGDKIIFGKYSGQTVKADGEELLVMREEDIFGIVEK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ~~mp.tement(77. .367)
/gene="NMB1973"
/note="similar to SP:P77913 PID:1513097 percent identity:
98.96, identified by sequence similarity; putative"
/codon_start=1
/transl_table=11
/prodin+----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="This region contains a gene with one or more premature stops or frameshifts, and is not the result of sequencing artifact; similar to GB:x59756 percent identify: 82.61; identified by sequence similarity; putative; IS1016C2 transposase, degenerate"
                                                                                                              Tettelin, H., Saunders, N.J., Heidelberg, J., Jeffries, A.C.,
Tettelin, H., Saunders, N.J., Heidelberg, J., Jeffries, A.C.,
Tettelin, H., Saunders, N.J., Ketchum, K.A., Hood, D.W., Peden, J.F.,
Dodson, R.J., Nelson, W.C., Gwinn, M.L., DeBoy, R., Peterson, J.D.,
Hickey, E.K., Haft, D.H., Salzberg, S.L., White, O., Fleischmann, R.D.,
Dougherty, B.A., Mason, T., Clecko, A., Parkesy, D.S., Blair, E.,
Cittone, H., Clark, E.B., Cotton, M.D., Utterback, T.R., Khouri, H.,
Qin, H., Vamathevan, J., Gill, J., Scarlato, V., Masignani, V.,
Pizza, M., Grandi, G., Sun, L., Smith, H.O., Fraser, C.M., Moxon, E.R.,
Rappuoli, R. and Venter, J.C.
Complete genome sequence of Neisseria meningitidis serogroup B
strain MCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /transl_table=11
/product="sodium- and chloride-dependent transporter"
/protein_id="AAR42303.1"
/db_xref="G1:7227236".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="similar to GB:L42023 SP:P44849 PID:1005680 PID:1220824 PID:1204983 percent identity: 77.47; identified by sequence similarity; putative"
                                meningitidis
Proteobacteria; beta subdivision; Neisseriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Neisseria meningitidis"
/strain="MC58"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="chaperonin, 10 kDa"
/protein_id="AAF42302.1"
/db_xref="GI:7227235"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 287 (5459), 1809-1815 (2000) 20175755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="serogroup: B"
complement(77, 367)
/gene="NMB1973"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:487"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="NMB1974"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1460. .2995
/gene="NMB1975"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="NMB1975"
Neisseria meningitidis.
Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 10619)
Tettelin, H., Saunders
                                                                                          Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
                                                                                                                              REFERENCE
                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
```

gene

CDS

```
/translation="MAQLPLYLESEIKDFTVGTPKVLESFSKHIPYGVVFEDDGDTGY
FYAASQDGILDALHIYNVEDVSDKHIPNHVLILWDDACTIAALCINDYIHAVYDFVEQ
AGYCRNGFPEAGGEWVKVENRVLDDELLDKILSRKST"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MPLLDSFKVDHTRMHAPAVRVAKTWTTPKGDTITVFDLRFCVPN
KEILPGKGIHTLEHLFAGFMRDHLNGNGVEIIDISPWGCRTGFYMSLIGTPSEQQVAD
AWLASMQDVLNVKDQSKIPELNEYQCGTYQMHSLAEAQQIAQNVLARKVAVNKNEELT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /hote="similar to GB:J01663 SP:P00582 GB:J01664 GB:V00317 PID:147312 percent identity: 68.19; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPVLVIGQVEADDVICTLAKQGAEHGLRVIVSTGDKDMAQLVDERVTLVNTMSSETLD
IEGVKAKFGVRPDQIRDYLALMGDKVDNVPGVEKCGPKTAVKWLEAYGSLAGVMEHAS
EIKGKVGENLQAALPQLPLSYDLVIIKTDVDLHAELSDGIESLRRTTPKWAQLVVDFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VTTEAQFAALLDKLSRADTIGIDTETTSLDAMNASLVGISIAFQAGEAVYIPVGHSLT
APEGLIDLODVLGRLKPHLGNPALKKIGONLKYODHVFANYGTALNGIAGDAMLASYI
IESHLGHGLDELSERMLGLETTYTSGLCGKGAKQIGFADVAIGQATEVAAQDEFALK
LEAHLRAQMDEKQLEMYEKMELPVAQVLFEMERNGVQIDRAELARQSAELGAELMKLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC015424 133144 bp DNA HTG 16-NOV-1999
Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered
pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MSNRPTLLLVDGSSYLYRAYHAMGQNLTAPDGAPTGALYGVLNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LRRLRSEYPHDYCAVVFDAKGKNFRHQMFEEYKATRPPMPDDLRPQAEALPDLVRLTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RWGFRTWLKEAESNMNTGSTDDLFGSDSIGEQAALNAEMPFEKQAEKATAPEKLDYQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4586 GCATCTTAAACAAAAAACACGCAAAAAAGCTATGACGGAAAGCGAAAGCGAATTTATCCGCGCG 4645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4646 AGCGAAGCATTATTTGAACACATCGAAGACCAAATCGACGAAAACGGCTGGGATTTCGAC 4705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cgtaaaccggtaacgcatcacctgacggaagaaatgcaaaaagagtttcattacaccatt 307
                                                                                                                                                                                                                                                                                                                                                                                                            6449. .6955
/gene="NMB1981"
/note="conserved hypothetical protein; identified by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                 /note="conserved hypothetical protein; identified by Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gaataacatatgaaatggttggaagaatccattatggccaaacgcggtgttggtgccggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Length 10619;
                                                                                                                                                                                  /product="conserved hypothetical protein"
/protein_id="AAF42308.1"
/db_xref="GI:7227241"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="conserved hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            308 ggcccttattccacacccgtcctgaccatcgaacccggtgaccg 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 39.2; DB
Pred. No. 3.6;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="DNA polymerase I"
/protein_id="AAF42310.1"
/db_xref="GI:7227243"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="AAF42309"
/db_xref="G1:7227242"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                    /gene"NMB1981"
/449. .6955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LDEGLLNA"
7101. .9917
/gene="NMB1982"
7101. .9917
                                                                                                                                                               /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7101. .9917
/gene="NMB1982"
                                 6008. .6427
/gene="NMB1980"
/gene="NMB1980"
6008. .6427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
AC015424/c
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
                                                                                                                                                                                                                                                                                                                                                             gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                                                                                                                                            CDS
                              CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              õ
CIYYAVIIGWAASYTYYSVNAAWGADPQGFFFKDFLQMAGPEALGLDFVGKVAGPLAG
VWVFTAAIMALGVQKGVARASSFFWPLLLVWFLIMVGISLTIPGGAAKGLDALFTPDWS
KLADSKVWVAAYGQIFFSLSICFGIMVTYSSYLKKKTDLGGTGLVVGFANSSFELLAG·
                                                                                                                                                                                                                                                                                                                                                                                                                             /product-"diaminopimelate decarboxylase"
/protein_id="AAR42304.1"
/db_xref="GI:2727237"
/translation="WTLFCEQVPYPRLAEAFGTPLYVYSQSALTEAFEHYQTAFAALN
PLOYAVAKARONLSIIKHFASLGSQFYDYSGGELARVLAAGGDAAKTFSGYGCKSEAE
IEFALNAGYKCFNAESIFETDGRYDALAGKTAPYSLRINPDVDAKTHPYTSTGLKA
NKFGIAYADALEAYHYAAQQPNLKIIGIDCHIGSQLTDLSPLVEACERILILVDALAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="G1:727239"
/translation="MMTESEFIRASEALFEHIEDQIDENGWDFDCRFAGNVLTIEAGD GAQIIVNRHTPNQELWIAAKSGGYHFAEQNGKWLATRDGRDFYDVLNEALSAASGEAV
                                                                              IGVFAALGFWAQAGGKAVNEVASGGIGLAFIAFPTIINQAFWGWLIGILFFGSLVFAG
YRAISILETYVAALQDKLWIGRVNATLVOCIPWGIVSTLEGTAFGLEVLDVWDKFV
NTVGIVAAGFVVVAT IIGSRLPERKHLMLSSIFIGGLWTVCVVTVVMLGYMLFK
DTSGLMEKNYEGYPDGFLSIFGWGMSAALVVFGLLLSLLPWKHGQDFNVKDEHBHEQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BGIVLEHLDIGGGVGIVYQDENVPDIGAYAQAVQKLIGTRRLKLILEPGRSLVGNAGS
LITRVERVKYGEKNEYMDAAMDLARPALYDAYHHIEAVETKDIATLTANIYGPIC
ELGDFLGKDPTIACEBGLLLLIRSAGAYGASMASNYNARNRAAEVLVDGNEYRLIRRR
ETLEQOMANELACLQAEHQNAV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MKYGVFFAAATALLLSACGYKGDLYLPKEGDKARFGVIQTGLQL
QSKPQSAPQTQK"
4616. .4939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISTEFFTALLGIRYLKMDKQLVYLTGAGCSICGAAAVMAAEPVTKAESHKVSVAIAVV
YIGGTLAIFTYPLFYTWGULTANGOGSIVGGSYUBVAGVYATGENDDIVAMTAVI
SKMIRVMMLAPFLLLMLSWLLTRSNGVSENTSHKTTIPWFAVLFIGVAIFNSPDLLPKE
LVKLFVEIDSFLLISSMAALGLTTQASAIKKAGLKPFVLGILTYLWLVVGGFLVVNGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="GI:7227240"
/translation="MNTRPFYFGLIFIAIIAILANYLGNTDFSHHYHISALIIAILLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAIGNTIYPQFSTQVEKGVLFAKGALLRTGIVLYGFRLTFGDIADVGLNAVVTDAIML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="NMil978"
/gene="similar to GB:L42023 PID:1573739 percent identity:
66.02; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                   /note="similar to SP:P19572 percent identity: 74.50; identified by sequence similarity; putative" /codon_start=1 /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="hypothetical protein; identified by Glimmer2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note-"conserved hypothetical protein; identified by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="conserved hypothetical protein"
/protein_id="AAF42307.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="hypothetical protein"
/protein_id="AAF42305.1"
/db_xref="GI:7227238"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="cyax protein"
/protein_id="AAF42306.1"
                                                                                                                                                                                                              complement(3120. .4364)
/gene="NMB1976"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(4375. .4545)
/gene="NMB1977"
complement(4375. .4545)
                                                                                                                                                                                                                                                                         complement(3120. .4364)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glimmer2; putative'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .yob. .5982
/gene="NMB1979"
4966. .soo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="NMB1978"
4616. .4930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4966. .5982
/gene="NMB1979"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="NMB1977"
                                                                                                                                                                                                                                                                                                  /gene="NMB1976"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .6427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EIAEL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6008.
```

gene

CDS

gene

CDS

ö

gene

CDS

gene

ACCESSION

```
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   782:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1657:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2992:
4107:
4127:
5424:
5444:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2972:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11635:
12453:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8724:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10385:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13164:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14007:
14027:
15565:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9550:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1638
29973
29973
4108
41128
5425
5445
61127
7389
7409
8745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10386
10406
11616
11636
12454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13165
13185
14008
14028
                                                                                                                                                                          TITLE
JOURNAL
REFERENCE
                                                                                                                                                                                                                                                        TITLE
JOURNAL
                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                              COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Light in y.

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Eukaryota; Metazoa; Arthropoda; Tracheata; Brachycera; Eukaryota; Meoptera; Endopterayota; Diptera; Brachycera;

I (bases 1 to 133190)

Muzny, D.M., Adams, C., Bailey, M., Barbaria, J., Blankenburg, K., Bodota, B., Bouck, J., Bowie, S., Brooks, A., Buanc, C., David, R., Delagado, O., Denazo, D., Ding, Y., Domah-Rashid, N., Dugan-Rocha, S., Durbin, K. J., Fernandez, C., Ferraguto, D., Guevara, W., Harris, K., Hernandez, J., Hodgson, A., Hogues, M., Kelly, S., Kondejewski, N., Konde, M., Gorrell, J. H., Gorrell, J. H., Jackson, L., Jia, Y., Jones, M., Lichtarge, O., Liu, J., Liu, W., Logan, O., Lozado, R., Lu, J., Lu, J., Lu, J., Lu, J., Lu, J., Lu, J., Lucler, R., Martinez, C., McLeod, M.P., Mei, G., Morgan, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ·;
                                                                                                                                                                                                                                                                              to fly@celera.com.
                                                            fruit fly.

Bukaryota; Metalongaster

Eukaryota; Metalongaster

Eukaryota; Metalongaster

Eukaryota; Metalong Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (Dases 1 to 133144)

Adams, M. and Venter, J.C.

Direct Submission

L. Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive,

Rockville, MD, USA

This sequence was identified as CDM:10214369 by the submitter.

For further information on this sequence e-mail to fly@celera.con

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* This sequence will be replaced

* Dy the finished sequence as soon as it is available and

Location/Qualifiers

I. 133144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17702 GGAGCTCTTCTTCTTCCGGGCGGGATGCGTCCATTGAACTCCTGCAGACGCTCCGGGC 17643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17642 GGCCGTAAAGTTGTCGTAGCGATCGCCAAACTCGTCCCCAAGTGGCCTCATGATCGCTCTG 17583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  320 acacccgtcctgaccatcgaacccggtgaccggattattgtcgacactcgagatgctttt 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          380 gaaggigetateaatteggaacaggatatteegageeagtigetaaaaatgeeetttete 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  440 aacccacaaaacggaccgatcatggtcaatggcgcggagaaaggtgatgtgctcgctgtc 499
                                                                                                            Hexapoda; Insecta;
                                                                                                                                                                                                                                                                the submitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster clone RPC198-6L11, *** SEQUENCING IN PROCESS ***, 70 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 133144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.7%; Score 39.2; DB 42; Length
49.1%; Pred. No. 5.8;
Live 0; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                              /organism="prosophila melanogaster"
/db_xref="taxon:7227"
41011 a 26133 c 25910 g 40090 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 17582 GTACTCGGCCTCATCCTCGCCCGTCGAGGTCA 17551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             500 tatatcgaatccatgttgccccgcgggcgttga 531
AC015424
AC015424.1 GI:6435911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC010003.5 GI:6996673
HTG: HTGS_PHASE1.
fruit fly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   133190 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.7
Best Local Similarity 49.1
Matches 104; Conservative
                                            HTG; HTGS_PHASE2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC010003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC010003
                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
                                                                                                                                                  REFERENCE
                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                        JOURNAL
                                      KEYWORDS .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC010003/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOURCE
ORGANISM
                    VERSION
                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                              COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                    SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rocus
```

q ô

Qy g

qq ò

δλ

```
Submitted (11-SEP-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor plaza, Houston, TX 77030, USA On Feb 18, 2000_this sequence version replaced gi:5902251.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing Vector: M13; L08821
Chemistry: Dye-primer Bodipy: 15% of reads
Chemistry: Dye-terminator Big Dye: 43% of reads
Assembly Program: Phrap; version 0,980611
Consensus quality: 77406 bases at least 040
consensus quality: 108419 bases at least 020
Estimated insert size: 120294; sum-of-contigs estimation
Quality coverage: 1.8x in 020 bases; sum-of-contigs estimation
                                      Oswal,G., Parish,B., Paxton,S., Payton,B., Perez,L., Pu,L.L.,
Qulles,M., Reiter,D., Rives,M., Samuel,S., Say,J., Scherer,S.,
Shah,E., Shen,H., Simon,M., Sparks,A., Stamps,A., Sucgang,R.,
Tabor,P., Taylor,T., Vasquez,L., Vinson,R., Vo,O., Wahbah,M.,
Watlington,S., Weinstock,G., Weinstock,I.R., Williamson,A.,
Cibhay,K., Wren,J., Wrensford,G., Yu,W., Zhou,X., Nelson,D. and
Morris,S., Nash,S., Nelson,A., Nguyen,R., Nguyen,N., Nguyen,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 70 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2: contig of 782 bp in length
7: contig of 835 bp in length
7: gap of unknown length
7: gap of unknown length
7: contig of 1315 bp in length
7: contig of 1315 bp in length
7: contig of 1315 bp in length
7: contig of 1125 bp in length
7: contig of 1125 bp in length
7: contig of 1297 bp in length
7: contig of 1297 bp in length
7: contig of 1297 bp in length
7: contig of 1242 bp in length
8: gap of unknown length
8: gap of unknown length
7: contig of 1316 bp in length
7: contig of 815 bp in length
7: gap of unknown length
7: contig of 1210 bp in length
7: contig of 1210 bp in length
7: contig of 1210 bp in length
7: contig of 815 bp in length
7: gap of unknown length
7: contig of 815 bp in length
7: gap of unknown length
7: contig of 813 bp in length
7: gap of unknown length
7: contig of 813 bp in length
7: gap of unknown length
7: contig of 823 bp in length
7: gap of unknown length
7: contig of 823 bp in length
7: gap of unknown length
7: contig of 823 bp in length
7: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown length
of 1538 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: BayYor College of Medicine
Center code: BCM
Center code: BCM
Contact: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center project name: DRAK
Center clone name: RPC198-6L11
Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---- Genome Center
                                                                                                                                                                                                                                                                          Gibbs, R.
Direct Submission
Unpublished
2 (bases 1 to 133190)
Worley, K.C.
Direct Submission
```

```
f unknown length
g of 1234 bp in length
f unknown length
g of 1334 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        f unknown length
g of 1606 bp in length
t unknown length
g of 1357 bp in length
t unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 f unknown length
g of 1825 bp in length
f unknown length
g of 890 bp in length
f unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g of 1627 bp in length
f unknown length
g of 1799 bp in length
f unknown length
g of 1488 bp in length
f unknown length
g of 1345 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       f unknown length
g of 2683 bp in length
f unknown length
g of 2161 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  f unknown length
g of 1913 bp in length
f unknown length
g of 2541 bp in length
                                                                                                                                                                                                                                                                                                                                                                                         bp in length
length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of 904 bp in length
unknown length
of 2083 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown length
of 1610 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown length
of 1286 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown length
of 1458 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown length
of 1607 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bp in length
length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bp in length
length
                                                                                                                                                                                                          of 1180 bp in length
                                                                                                                                                                                                                                                                         of 1251 bp in length
                                                                                                                                                                                                                                                                                                     unknown length
of 1231 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of 1662 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of 625 bp in length
unknown length
                                                                                       of 973 bp in length
unknown length
of 832 bp in length
                                  of 984 bp in length
unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown length
                                                                                                                                                                                                                                                                                                                                                                length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 length
                                                                                                                                                                                     unknown length
                                                                                                                                                                                                                                             unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        length
                                                                                                                                                                                                                                                                                                                                                                                                                                                        of 1083 h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown
of 1110 h
                                                                                                                                                                                                                                                                                                                                                                   unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of 1139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gap of contig capp of contig capp of c
                                                                                                                                                                                                       contig
gap of contig
contig
                                                                                                                                                                                                                                                                                                                              contig
gap of contig
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                     contig
gap of contig
gap of contig
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig contig co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contig
gap of
contig
gap of
contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contig
gap of contig
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contig
gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       contig
gap of
                               contig
gap of
contig
gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70076:
70096:
                                                                                                                                                                                                                                                                                                                                                                                                                     23523:
24606:
24626:
25765:
25785:
26895:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31149:
32506:
32526:
33151:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34853:
36463:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36483:
37769:
37789:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48361:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64223:
64243:
66061:
66081:
                                                                                                                                                                                                                                       19634:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28149:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29503:
29523:
31129:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39267:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42002:
42022:
43649:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13669:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56915:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54462:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50212:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   224627
2256627
226627
226627
226627
226627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
227627
2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60213
62374
62394
64224
64244
66062
15566
16570
16570
17563
17563
17583
18415
18415
19615
20906
22137
                                                                                                                                                                                                                                                                                                                                                                                                                     23504
23524
24607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68234
68254
70077
```

```
fruit fly.

Drosophila melanogaster

Braxpota: Metazoa: Arthropoda: Tracheata: Hexapoda: Insecta;

Braryota: Metazoa: Arthropoda: Tracheata: Brachycera:

Pterygota: Neoptera: Endopterygota: Diptera: Brachycera:

Muscomorpha: Ephydroidea: Drosophilidae; Drosophila.

1 (bases I to 154381)

Muzny, D. M., Adams, C., Bailey, M., Barbaria, J., Blankenburg, K.,

Bodota, B., Bouck, J., Bowie, S., Brooks, A., Buhay, C., Bunac, C.,

Burkett, C., Burrows, J., Carter, M., Chacko, J., Chen, Z., Cox, C.,

David, R., Delgado, O., Deshaco, D., Ding, Y., Domah-Rashid, N.,

Buyan-Rocha, S., Durbin, R.J., Fernandez, C., Ferraguto, D.,

Forcum-Tansey, J., Frantz, P., Ganesh, R., Gorrell, J. H., Gorrell, L.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 1111107 ACCACGGGCTGGCTATCGGTATGCCAGACTGGATTATTGCTGCTGCTGGAGTGGTATT 111048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        320 acacccgtcctgaccatcgaacccggtgaccggattattgtcgacactcgagatgctttt 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              380 gaaggigctatcaattcggaacaggatattccgagccagtigctaaaaatgccctttctc 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster clone RPCI98-8G12, *** SEQUENCING IN PROCRESS ***, 74 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 133190;
                                    contig of 2897 bp in length contig of 2897 bp in length contig of 2427 bp in length contig of 2427 bp in length gap of unknown length length contig of 1897 bp in length contig of 1897 bp in length contig of 1897 bp in length gap of unknown length length contig of 3405 bp in length gap of unknown length contig of 3303 bp in length gap of unknown length contig of 229 bp in length gap of unknown length contig of 2029 bp in length gap of unknown length gap of unknown length contig of 2029 bp in length gap of unknown length contig of 2893 bp in length contig of 4075 bp in length gap of unknown length contig of 4075 bp in length gap of unknown length gap of unknown length contig of 4075 bp in length gap of unknown length contig of 4850 bp in length gap of unknown length gap of unknown length contig of 4850 bp in length gap of unknown length contig of 4850 bp in length gap of unknown length contig of 4850 bp in length gap of unknown length contig of 4850 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 5.8;
0; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 110927 GTACTCGCGCTCATCCTCGCCCGTCGAGGTCA 110896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 39.2; DF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       500 tatatogaatocatgttgccccgcggcgttga 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC009369.5 GI:6996666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.7%;
                                                                                                                80001:
80021:
81918:
81938:
                                                                                                                                                                                                                                                                                           90648:
93277:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154381 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                101783:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      105878:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116841:
                                                                                                                                                                                                                                                                                                                                                                                                                                101763:
                                                                                                                                                                                                 83880:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 2.7
Best Local Similarity 49.1
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTG; HTGS_PHASE1.
fruit fly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC009369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC009369/c
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

us-09-214-679-1.rge

TITLE JOURNAL

COMMENT

```
f unknown length
g of 1185 bp in length
f unknown length
of 1882 bp in length
f unknown length
g of 975 bp in length
                                                                                                                                                                                                                                                                                                            f unknown length
3 of 1425 bp in length
f unknown length
3 of 1428 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              op ...
length
'n length
                 in length
                          known length
1257 bp in length
                                                                                             unknown length
of 1282 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jp ...
length
'n length
                                                                                                                                                                                          unknown length
of 1182 bp in length
                                                                                                                                                                                                                                                                                     unknown length
of 1038 bp in length
                                                                                                                                                                                                                                                                                                                                                          unknown length
of 1190 bp in length
                                                                                                                                                                                                                                                                                                                                                                                  unknown length
of 1702 bp in length
                                                             of 820 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bp in length
length
                                                                                   of 976 bp in length
                                                                                                                                876 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                    of 1346 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                            bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bp in length
                                                   unknown length
                                                                                                                        unknown length
                                                                                                                                             unknown length
of 1323 bp in ]
                                                                           length
                                                                                                                                                                     unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown length
of 1792 bp in l
                                                                                                                                                                                                                                                                                                                                                                                                           length
                                                                                                                                                                                                                                                                                                                                                                                                                                                       length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ength.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ņ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of 1013 bp
                                                                                                                                                                                of 861 bp
                                                                        unknown
                                                                                                                                                                                                                                                                                                                                                                                                          unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
of 1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
of 1647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
of 1577 )
                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            contig of 2381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of 1124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of 1273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of 2845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of 2647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of 1434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of 2385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of 1504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown
                                                                                                                                   oĘ
                                                                                                                                                         of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oŧ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oť
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of
                                   contig
gap of 1
contig
gap of 1
contig
gap of 1
                                                                                                                               contig
gap of
contig
gap of
                                                                                                                                                                                                   contig
gap of
                                                                                                                                                                                                                                                                                                                                                          gap of contig
                                                                                                                                                                            contig
                                                                                                                                                                                                                                       gap of
contig
                                                                                                                                                                                                                                                                                                 contig
gap of
                                                                                                                                                                                                                                                                                                                                  gap of
                                                                                                                                                                                                                                                                                                                                                                                            contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                              gap of
contig
gap of
contig
gap of
contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gap of contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               contig
gap of
contig
gap of
                                                                                                                                                                                                                                                                          contig
                                                                                                                                                                                                                                                                                       gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contig
gap of
                                                                                                                                                                                           gap of
                                                                                                                                                                                                                                                               gap of
                                                                                                                                                                                                                                                                                                                          contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gap of
contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contig
gap of
contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                   gap of
                                                                                                                                                                                                                                                                                                                                                                                                                     contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         contiq
                                                                                                                                                                                         2391:
                                                                                                                                                                                                                                                                                                                                                           31646:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50833:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53480:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63044:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64853
           13465
14837
14857
16114
16134
16954
16974
17970
17970
119252
19252
19252
20168
20168
                                                                                                                                                                                       223372
223392
233544
234779
24779
24799
26681
26701
27676
27696
                                                                                                                                                                                                                                                                                                                     28754
30179
31627
31627
32857
34579
35925
35925
35945
37737
37757
37757
37757
37757
37757
41514
41514
41514
423111
45532
46656
47949
47949
47969
                                                                                                                                                                             11511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53481
53501
54935
57413
57413
57433
59818
61342
61342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63045
63065
          Holloway,C., Hosak,H., Jackson,L.E., Jackson,L., Jia,Y., Jones,M., Felly,S., Kondejewski,N., Kong,Y., Kovar,C., Leal,B., Li,Z., Lichtarge,O., Liu,J., Liu,W., Logan,O., Lozado,R.J., Li,Z., Lucier,R., Martin,R., Martinez,C., McLeod,M.P., Mei,G., Morgan,M., Morris,S., Nash,S., Nelson,A., Nguyen,R., Nguyen,R., Nguyen,R., Nguyen,R., Nguyen,R., Nguyen,R., Nguyen,R., Nguyen,R., Sah,E., Shen,H., Simon,M., Sparks,A., Stamps,A., Sucaers,S., Tabor,P., Taylor,T., Vasquez,L., Vinson,R., Vo,Q., Wahbah,M., Watlington,S., Weinstock,G., Weinstock,I.R., Williamson,A., Glibbs,R., Ren,J., Weensford,G., Yu,W., Zhou,X., Nelson,D. and
                                                                                                                                                                                                   Direct Submission
Submitted (20-AUG-1999) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Feb 18, 2000 this sequence version replaced gi:5881432.
Center: Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                                                              Chemistry: Dye-primer Bodipy: 42% of reads
Chemistry: Dye-primer Bodipy: 42% of reads
Assembly program: Phrap: version 0.980611
Consensus quality: 100833 bases at least 040
Consensus quality: 122674 bases at least 030
Consensus quality: 132575 bases at least 030
Estimated insert size: 144035; sum-of-contigs estimation
Quality coverage: 2.1x in 020 bases; sum-of-contigs estimation
Guevara,W., Harris,K., Hernandez,J., Hodgson,A., Hogues,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 74 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            f unknown length
g of 1169 bp in length
f unknown length
g of 887 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inknown length
g of 836 bp in length
...known length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown length
of 1250 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1022 bp in length
nown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of 782 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    888 bp in length
known length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of 921 bp in length
                                                                                                                                                                                                                                                                                               Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc.help@bcm.tmc.edu
Project Information
Center project name: DRAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
of 1022
                                                                                                                                                                                                                                                                                                                                                 Center clone name: RPC198-8G12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
                                                                                                                                                                                                                                                                                                                                                          Sequencing vector: M13; L08821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contig
gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contig
gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gap of
contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       contig
gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             contig
gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gap of
                                                                                                                                                    Direct Submission
Unpublished
2 (bases 1 to 154381)
                                                                                                                                                                                                                                                                                        Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1658:
2546:
3735:
3755:
4642:
4662:
5583:
6853:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     895:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10559:
11902:
11922:
13444:
                                                                                                                                                                                         Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1639
25547
25547
25547
3736
3736
4663
3756
6874
6874
6874
6874
6874
8958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10540
10560
11903
11923
13445
                                                                                                                                                                           REFERENCE
AUTHORS
TITLE
JOURNAL
```

```
if unknown length
ig of 2380 bp in length
ig of 2733 bp in length
ig of 2733 bp in length
if unknown length
if unknown length
ig of 2355 bp in length
ig of 3364 bp in length
ig of 1418 bp in length
ig of 1418 bp in length
ig of 2006 bp in length
if unknown length
ig of 2006 bp in length
ig of 2364 bp in length
ig of 2364 bp in length
ig of 2364 bp in length
ig of 2810 bp in length
ig unknown length
                                                                              g of 2750 bp in length
f unknown length
g of 1976 bp in length
unknown length
g of 1881 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of 2766 bp in length
unknown length
of 2906 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown length
of 3246 bp in length
unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown length
of 2288 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gap of unknown rengementing of 4807 bp in length
                            in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of 2945 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown length
                               contig

gap of

contig

gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contig
gap of
contig
gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109213:
112158:
112178:
116985:
                                                                                                                                                                                                                                             81017:
81037:
83770:
83790:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03619:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03639:
70649
70669
71971
71971
74721
74721
74721
76737
78618
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
81018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103640
106886
106906
109194
112159
```

ö 0; Gaps DB 51; Length 154381; Query Match 2.7%; Score 39.2; DB 51; Length Best Local Similarity 49.1%; Pred. No. 6; Matches 104; Conservative '0; Mismatches 108; Indels

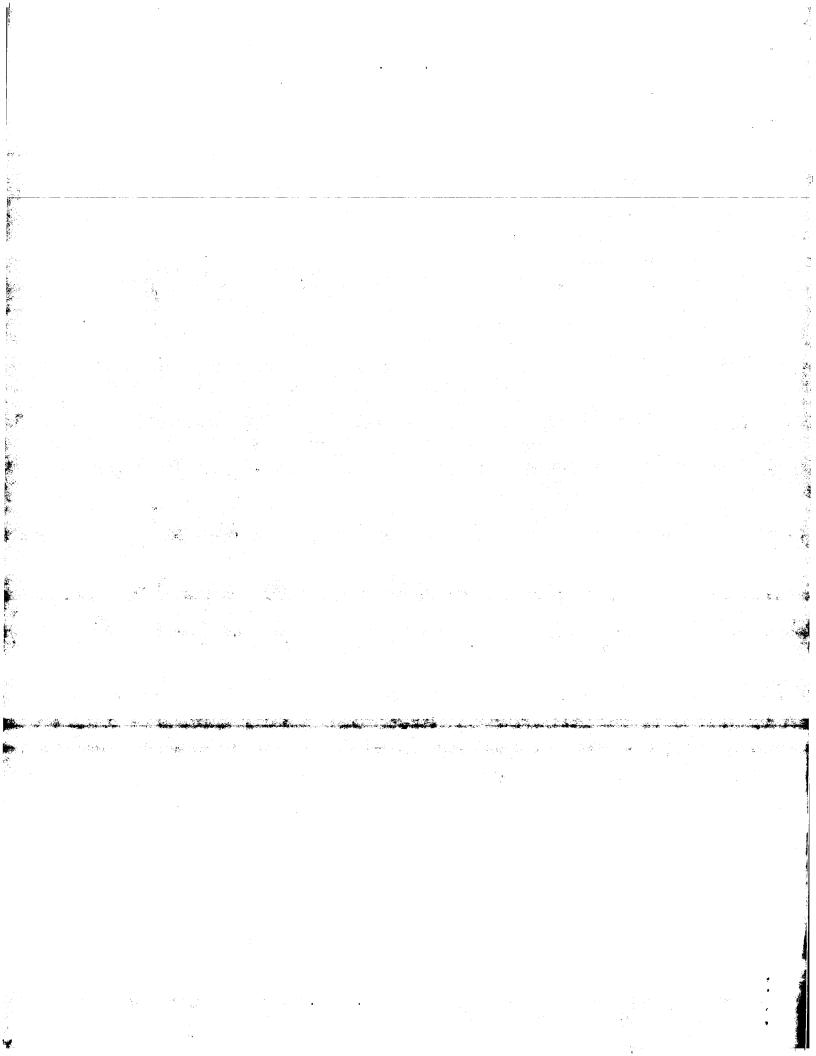
440 aacccacaaaacggaccgatcatggtcaatggcgcggagaaaggtgatgtgctcgctgtc 499 οy

DD 139913 GGCCGTAAAAGTTGTCGTAGCGATCGCCCAAACTCGTCCCCAAGTGGCCTCTG 139854

500 tatatcgaatccatgttgccccgcggcgttga 531 δ

Db 139853 GTACTCGCGCTCATCCTCGCCCGTCGAGGTCA 139822

Search completed: September 9, 2000, 21:26:31 Job time: 4169 sec



```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM nucleic - nucleic search, using sw model

September 9, 2000, 20:18:12; Search time 67.18 Seconds (without alignments) 5370.303 Million cell updates/sec Run on:

US-09-214-679-1 1442 1 cccgggaactccatgtggcc.....aatgcaattcatttggatcc 1442 Title: Perfect score: Sequence:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

623170 Total number of hits satisfying chosen parameters: 311585 seqs, 125096042 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N\_Geneseq\_36:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARTES

		Description	K. oxytoca R-speci	death	Cell death hid gen	Human CYP3A4 gene		H. pylori GHPO 166	Alpha-1,4-glucan l	M.costata DNA enco	Morchella costata	EST clone HO266. N	K.lactis transaldo	K.lactis transaldo	Human hepatocyte n	Encodes protein ho	<ul><li>P. aeruginosa dete</li></ul>	Rhizobium species	Rhizobium species	ซ		E. coli lacI methy	Chloramphenicol re	Neutral protease n	E	DNA encoding a Sta	Staphylococcus aur	Enterococcus faeca	Papaya ACC synthas	DNA encoding a S.	Human epididymis-s	Streptococcus pneu	H. pylori cytoplas	片	T. niveum Cyclospo
SUMMARIES		£ £	V10449	066950	Q66948	x28300	X00477	X14578	089701	Q87616	V84194	V88779	Q57702	057701	V52729	048718	T28490	V30458_0	on.	V52023	T39536	T39535	V12274	093164	V58938	V53317	V74380	x13159	V31482	V65258	T97955	V52245	T67858	x13020	054386
		DB I															_								_										
		Match Length		3900	502	429	5733	745	3201	3201	3201	383	1226	1349	6260	618	2167	110000	110000	1443	1187	1188	1542	1049	10095	417	7494	11597	1888	2221	4665	7902	1620	17250	46895
ø	Query	Match			5.6		٦.	2.3	٠,	2.3							2.5				•		•					2.1					2.0		
		Score	1442	39.2	37.6	35.2	34.2	33.2	33.2	33.2	33.2	32.8	32.2	32.2	32.2	31.6	31.2	31.2	31.2	31	30.8				30.2								29.5		
	Result	No.	Т	7	c	4	S	9	7	8	σ	10	11	12	13	14	15	16	11	18	19	20	21	22	23	24	52	56	27	28	29	30	31	32	33
	Res	;		υ	O	ပ	٠		Ų	υ	U		υ	ပ									U	O			ပ	O		ပ	ပ		U		

Continuation (5 of	Continuation (5 of	N. qonorrhoeae-spe	Sequence specific	Neisseria gonorrho	Neisseria gonorrhe	Corticosterone-bin	Enterococcus faeca	DNA encoding a ccM	Mycobacterium spec	Staphylococcus aur	Enterococcus faeca	
V30458_4	V30459_4	T34990	Q51201	T34986	V33485	052699	X12956	X34596	X34232	X19481	X13046	
н	-1	Н	Н	-	Н	Н	Н	Н	-	-	-	
110000	110000	300	850	850	1067	3596	25580	1479	1023	2019	2350	
2.0	5.0	7.0	2.0	2.0	7.0	2.0	2.0	7.0	7.0	2.0	2.0	
29.3	29.2	29	29	53	29	29	29	28.8	28.6	28.6	28.6	
34	32	36	37	38	39	40	41	42	43	44	45	
									U	U	O	

## ALIGNMENTS

181 acgtggagaataacatatgaaatggttggaagaatccattatggccaaacgcggtgttgg 240

δλ

2

```
RESULT
066948/c
                                                                                                                                                                                                                                                                              a
                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                     οŽ
                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                              ŏ
                                                                                                                                                                                                                                                                                                           1200
                                                                                                                                                                                                                                                                                                                     1200
                                                                                                                                                                                                                                                                         300
                                                                   cgacactcgagatgcttttgaaggtgctatcaattcggaacaggatattccgagccagtt 420
                                                     900
                                                                                                                                                                                                                                                                                                                                                cagotaaaagcaggtgcatatggggccagatacacccatcaatattggtttactttactcc 1320
                                                                                                                              099
                                                                                                                                       099
                                                                                                                                                 720
                                                                                                                                                     840
         ACGTGGAGAATAACATATGAAATGGTTGGAAGAATCCATTATGGCCAAACGCGGTGTTGG
                                                                                                                                                                                                                                                caccattggcccttattccacacccgtcctgaccatcgaacccggtgaccggattattgt
                                                                                                                             caatgatccgctgccagaaaaggtgcgcatgattaaactcgacagtgaaaaggtctactg
                                                                                                                                               gagcaaacgccatacgcttccctataaaccccatattggcaccttgagcgtatcgccaga
                                                                                                                                                                                      aattgcatatcgcgacttaatttactggctggtagaagactttggcttcgaacaatggga
                                                                                                                                                                                                                                                                                      tgcctacatgcttctgagtcaatgcggcaaagtgcggctgggcaacatggtcgacccaa
181
                                                         361
                            301
                                      301
                                                361
                                                                                                481
                                                                   421
                                                                             421
                                                                                                                   541
                                                                                                                             601
                                                                                                                                                                            721
                                                                                                                                                                                                                                                                   1021
                                                                                                                                                                                                                                                                             1021
                                                                                                                                                                                                                                                                                               1081
                                                                                                                                                                                                                                                                                                         1141
                                                                                                                                                                                                                                                                                                                   1141
                                                                                                                                                                                                                                                                                                                                               1261
                                                                                                          541
                                                                                                                                      601
                                                                                                                                                199
                                                                                                                                                         199
                                                                                                                                                                   721
                                                                                                                                                                                               781
                                                                                                                                                                                                         841
                                                                                                                                                                                                                   841
                                                                                                                                                                                                                             901
                                                                                                                                                                                                                                                961
                                                                                                                                                                                                                                                          961
                                                                                                                                                                                                                                                                                      1081
                                                                                                                                                                                                                                                                                                                            1201
                                                                                                                                                                                                                                                                                                                                      1201
                                                                                                                                                                                                                                                                                                                                                         1261
                                                                                      481
                                                                                                                                                                                      781
                                                                                                                                                                                                                                      901
g
         ò
                  d
                            οy
                                     g
                                                        g
                                                                                              q
                                                ò
                                                                   δy
                                                                            q
                                                                                      òγ
                                                                                                         ò
                                                                                                                  ď
                                                                                                                            Ω
                                                                                                                                     g
                                                                                                                                               ò
                                                                                                                                                        рp
                                                                                                                                                                   ōλ
                                                                                                                                                                           g
                                                                                                                                                                                              a
                                                                                                                                                                                                         ò
                                                                                                                                                                                                                   g
                                                                                                                                                                                      Qγ
                                                                                                                                                                                                                             δλ
                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                δλ
                                                                                                                                                                                                                                                                  Ω
                                                                                                                                                                                                                                                                            qq
                                                                                                                                                                                                                                                                                              Ω
                                                                                                                                                                                                                                                       임
                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                         δy
                                                                                                                                                                                                                                                                                                                  a
                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                            ŏ
```

```
ö
                                                                                439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acaccegtectgaccategaacceggtgaceggattattgtegacaetegagatgetttt 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      440 aacccacaaaacggaccgatcatggtcaatggcgcggagaaaggtgatgtgctcgctgtc 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig. 6; 93pp; English.

The reaper (rpr) and head involution defective (hid) genes, mapping to position 75C1,2 of D. melanogaster chromosome 3, exhibit expression patterns related to the pattern of cell death during Drosophila embryogenesis. Cell death genes, or antisense sequences, can be used to reduce or abolish apoptosis, e.g. in transgenic animals. An hid cDNA sequence is given in 060590, and the deduced sequence of the encoded HID protein in R55791.
Sequence 3900 BP; 1288 A; 876 C; 736 G; 1000 T;
                  ttcagcggagtgacggcggcacaagagttgtcacaatggcgcggagcaacccaggctatt
                                                                                                                                                                                                                                                                                                             gene; reaper gene; rpr;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1458 ACCACCGGACTGGCTGTGTGTGGCAGATTATTGCTGCTGGTGGCTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gaaggtgctatcaattcggaacaggatattccgagccagttgctaaaaatgccctttctc
                                                               gccgaaattaatcaaaatggcggcatcaacggcagaccactcaatgcaattcatttggat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated cell death genes from Drosophila - and novel assays for apoptotic cell deaths and apoptotic and necrotic cell deaths, based on selective staining by toluidine blue, acridine orange
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 49.1%; Pred. No. 0.0077;
49.1%; Pred. No. 0.0077;
4; Conservative 0; Mismatches 108; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    χ.
                                                                                                                                                                                                                                                                    T5-FEB-1995 (first entry)
Cell death hid cDNA.
Cell death, head involution defective; hid graphotosis; transgenic animal; antisense; ss.
Drosophila melanogaster.
Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  White
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MASI ) MASSACHUSETTS INST TECHNOLOGY.
Abrams JM, Grether ME, Steller H, W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   500 tatatogaatocatgttgccccgcggcgttga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1278 GTACTCGCGCTCATCCTCGCCCGTCGAGGTCA
                                                                                                                                                                                                                                           BP.
                                                                                                                                                                                                    RESULT 2
Q66950/c
ID Q66950;
AC Q66950;
AC — mm-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                        400. .1632
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1994.
14-JAN-1994; U00500.
15-JAN-1993; US-004957.
17-SEP-1993; US-123343.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 94-249218/30.
P-PSDB; R55791.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and Nile blue
                                                                                                                                                            1442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Simil
Matches 104; C
                                                                                                                            cc 1442
                                                                                                                                                                                                                                                                                                                                                                                                      WO9416071-A
                                                                                                                                                  _
::
1321
                                                                                                                            1441
                                                                                                                                                            1441
                                                              1381
                                                                                            1381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        380
                          셤
                                                            δ
                                                                                          a
                                                                                                                            δλ
```

```
P-PSDB; W30607
                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US5859338-A.
                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          intron
                                                                                                                                                                                                                                                                                                                                                                                        S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             exon
                                                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                    X00477
 à
                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-JUN-1999 (first entry)
Human CYP3A4 gene exon 7, intron 7.
CYP3A4 gene polymorphism; polymorphic locus; human; altered metabolism;
CYP3A4 substrate; drug-drug interaction identification; toxin exposure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          acacccgtcctgaccatcgaacccggtgaccggattattgtcgacactcgagatgctttt 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        380 gaaggtgctatcaattcggaacaggatattccgagccagttgctaaaaatgccctttctc 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                Disclosure: Fig.5; 93pp; English.

The reaper (rpr) and head involution defective (hid) genes, mapping to position 75C1.2 of D. melanogaster chromosome 3: exhibit expression patterns related to the pattern of cell death during Drosophila embryogenesis. Cell death genes, or antisense sequences, can be used to reduce or abolish apoptosis, e.g. in transgenic animals. The genemic sequence of hid is given as 4 contiguous sequences in Q66946-49, which together encode HID protein.
Sequence 502 BP; 141 A; 135 C; 135 G; 90 T;
                                Cell death hid gene.
Cell death; head involution defective; hid gene; reaper gene; rpr;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    440 aacccacaaaacggaccgatcatggtcaatggcgcggagaaaggtgatgtgctcgctgtc
                                                                                                                                                                                                                                     Isolated cell death genes from Drosophila - and novel assays for apoptotic cell deaths and apoptotic and necrotic cell deaths, based on selective staining by toluidine blue, acridine orange and Nile blue
                                                                                                 /*tag= a
/note= "Base n at position 93 is not identified
in the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                    ó
                                                                                                                                                                                                                                                                                                                                                                                                              Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genetic linkage detection; phenotypic variation; intron; ss.
Homo sapiens.
WO9913106-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                    109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            Score 37.6; DB 1;
Pred. No. 0.0072;
0; Mismatches 109;
                                                                                                                                                                                                     White K;
                                                      apoptosis; transgenic animal; antisense; ss.
Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               500 tatategaateeatgttgeeeegggggttga 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    153 GTACTCGCGCTCATCCTCGCCCGTCGAGGTCA 122
                                                                                                                                                                                           (MASI ) MASSACHUSETTS INST TECHNOLOGY
                                                                                                                                                                                                      Grether ME, Steller H,
                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                              2.6%;
Q66948 standard; DNA; 502 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X28300 standard; DNA; 429 BP.
                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-MAR-1999.
02-SEP-1998; U18158.
10-SEP-1997; US-058612.
(AXYE-) AXYS PHARM INC.
Guida M, Lichter JB;
                                                                                                                                                                   15-JAN-1993; US-004957.
17-SEP-1993; US-123343.
                                                                                                                                                         14-JAN-1994; U00500.
                                                                                                                                                                                                      Abrams JM, Grether
WPI; 94-249218/30.
                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                      misc_difference
                                                                                                                                                                                                                           P-PSDB; R55790
                    15-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Sim:
Matches 103;
                                                                                                                                  W09416071-A
                                                                                                                                               21-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                        320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X28300/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC
DT
DE
DT
DE
PD
PD
PD
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
```

```
ö
                                                                                                                                                       which is part of a non-naturally occurring chromosome. Nucleic acids comprising the CYPBA4 polymorphic sequences can be used to screen patients for altered metabolism for CYPBA4 substrates, potential drug-drug interactions, and adverse/side effects as well as diseases that result from environmental or occupational exposure to toxins. They can also be used to establish animal, cell culture and in vitro cell-free models for drug metabolism. Polymorphic CYPBA4 gene sequences can be used for expression studies to determine the effect of promoter and/or intron sequence variations on maRNA expression and stability. The polymorphisms are also used as single nucleotide polymorphisms to detect genetic linkage to phenotypic variation in activity and expression of CYPBA4. The nucleic acids can also be used to generate genetically modified non-human similars or site specific gene modifications in cell lines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       thaliana. The nucleotide sequence encoding CLVI, including its corresponding antisense sequences, are used to alter meristem phenotypes, in particular the enlargement of apical shoot or floral meristems, to provide an increased yield of leaves, flowers, fruits and seeds in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence encodes clavatal (CLV1) isolated from Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1164 acaaaaacctgttagtttagtaggaataactaaccggtgaacattacccggatgtagatc 1223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana clavatal encoding DNA.
Arabidopsis thaliana; clavatal; CLV1; meristem phenotype; harvesting; apical shoot enlargement; floral meristem; resistance; ss.
Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 related vectors, plant cells and plants - used to regulate meristem phenotype, for increasing yield of leaves, flowers, fruits and seeds Claim 3; Fig 5; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated nucleic acid encoding the plant clavatal protein and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.4%; Score 35.2; DB 1; Length 429; 57.5%; Pred. No. 0.044;
                                                             Disclosure; Page 30; 40pp; English.
This sequence represents an intron of the human CYP3A4 ge
The invention relates to a CYP3A4 sequence polymorphism,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1224 ggggtaatgtgtaagttcaaacaatcgctatttttaacagctaaag 1269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      255 ATGGTGATTATATCTCAATAAAGCAGTTATTTTAAAGAGAGMAAG 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
WPI; 99-215070/18.
New isolated CYP3A4 polymorphic sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2434. .5470
/*tag= a
/note= "contains introns"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CALY ) CALIFORNIA INST OF TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clark SE, Meyerowitz EM, Williams RW; WPI; 99-120031/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X00477 standard; DNA; 5733 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5118. .5470
/*tag= d
/number= 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .5038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5039. 5117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= c
/number=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /number-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-JAN-1999.
06-JUN-1995; 473553.
06-JUN-1995; US-473553.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2434.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 61; Conserv
```

```
RESULT 8
Q87616/c
ID Q87616 standard; DNA; 3201
                                                                                                                                                                                                                                                                                                                                               95-161802/21.
                                                                                                                                                                      27-DEC-1995
                                                                                        212
                                                                                                                                                                                                                                                                WO9510617-A.
                                                                356 at 357
                                                                                                                                                                                                                                                                                                                        Bojsen K,
Yu S;
                                                                                   AT.
                                                                                                                                                                                                                                                                                                              (DANI-)
                  296
                                                                                       211
                                        g
                                                                δŏ
                                                                                       엄
                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                             ó
 very wide variety of plants. They may also be used to increase resistance to lodging or wind damage, or to facilitate harvesting. Fragments of the nucleotide sequence encoding CLV1 are also useful as probes to identify
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                               X14578;
31-MAR-1999 (first entry)
H. pylori GHPO 1662 gene.
GHPO protein; Helicobacter infection; gastroduodenal disease; gastritis;
peptic ulcer disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated Helicobacter polynucleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter infections and gastrointestinal diseases claim 1; Page 1937-1938; 2054pp; English.

This sequence represents a polynucleotide of the invention. It was isolated from Helicobacter pylori and encodes a H.pylori GHPO protein. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroducdenal diseases associated with these infections, including acute, chronic, and atrophic gastritis, and peptic ulcer diseases. G. gastric and duodenal ulcers. They can also be used for the production and diagnosis.
                                                                                                                              1196 accggtgaacattacccggatgtagatcggggtaatgtgtaagttcaaacaatcgctatt 1255
                                                                                                                                                                                                 3769 ACTGATAATTTCTTCTCCGGTGAACTTCCGGTAACGATGTCCGGCGATGTTCTCGATCAG 3828
                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        176 aaattacgtggagaataacatatgaaatggttggaagaatccattatggccaaacgcggt 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gttggtgccgggcgtaaaccggtaacgcatcacctgacggaagaaatgcaaaaagagttt 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                    DB 1; Length 5733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 745;
                                                                                                                                                                                                                        1256 tttaacagctaaagcaggtgcatatggggccagatacacccatcaat 1302
                                                                                                                                                                                                                                      3829 ATTTACCTCTCTAACAACTGGTTTTCCGGCGAGATTCCACCTGCGAT 3875
                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Al-Garawi A, Kleanthous H, Miller C, Oomen RP, Tomb J;
WPI; 98-542293/46.
P-PSDB; W98859.
                                                 1094 G;
                                                                                                         83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JUL-1997; US-902615.
01-ARR-1997; US-813457.
24-JUN-1997; US-81227.
10MA-N GENOME SCI INC.
(INMR.) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           159
                                                                                ch 2.4%; Score 34.2; DB 1 Similarity 50.3%; Pred. No. 0.54; 84; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 33.2; DB Pred. No. 0.32;
                                 related sequences in other plants.
Sequence 5733 BP; 1732 A; 1144 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102 C;
                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                       X14578 standard; DNA; 745 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          265 A;
                                                                                                                                                                                                                                                                                                                                                                                                   37. .720
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            01-APR-1998; U06371
                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          745 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                         WO9843478-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89;
                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local 9
                                                                                                                                                                                                                                                                                  9
                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      236
                                                                                                                                                                                                                                                                                                                                                                                       Key
                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                          X14578
888888
                                                                                                                                                    g
                                                                                                                                                                            ŏ
                                                                                                                                                                                                  d
                                                                                                                                                                                                                         δλ
                                                                                                                                                                                                                                               рp
                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

```
While State of the Parameter of alpha-1,4-glucan lyase from fungus - and its recombinant prodn from isolated DNA.

For Isolation of alpha-1,4-glucan lyase from fungus - and its recombinant prodn from isolated DNA.

Claim 9; Pages 30-32; 51pp; English.

CC The enzyme alpha-1,4-glucan lyase(GL)was purified from Morchella costata (MC) by affinity chromoatography on beta-cyclodextrin costata (MC) by affinity chromoatography on beta-cyclodextrin costata (MC) in exchange on Mono Q HR 5/5 (FTM) and gel costatation on Sepharose (RTM) 12 columns. The purified enzyme an Isolectric point of pl 5.4. The optimum pH range for the fungal cost in a Isolectric point of pl 5.4. The optimum pH range for the fungal lyase catalysed reaction was between pH 5 and pH 7. The purified cost lyase catalysed reaction was between pH 5 and pH 7. The purified cost lyase catalysed reaction was between pH 5 and pH 7. The purified cost lyase catalysed reaction was between pH 5 and pH 7. The purified cost maltotriose (56%) and maltose (2%). The lyase was digestesd with condoproteinase Arg-C from Clostridium histolyticum or endoproteinase CC Lys-C from Lysobacter enzymogenes. The resulting peptides were componences of three overlapping cC Lyptic peptides from GL (se R72713) were used to generate mixed collyos which could be used as PCR primers for the amplification of CC DNA isolated from Morchella. The primers are 089703-4 and 090305-6.
cattacaccattggcccttattccacacccgtcctgaccatcgaacccggtgaccggatt 355
                                        151 GGGCATTCTATTAGCGTTCATTCTACCGATGATATTTCATCCAAACAGATGAAGAGGGT 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 ccgggcgtaaaccggtaacgcatcacctgacggaagaaatgcaaaaagagtttcattaca 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1028 CTGGGCTTCAACTTTGAACGTCCAACAAGACCTGTATAAAGTCGTACAATTTCCGGGACC 969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             303 ccattggcccttattccacacccgtcctgaccatcgaacccggtgaccggattattgtcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     968 GTATCCGCACTGATACCGTAACAATCGATACCACATACCTGGTTCCCAGCTTGATGTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 3201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      363 acactcgagatgcttttgaaggtgctatcaattcggaacaggatat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Marcussen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.3%; Score 33.2; DB 50.0%; Pred. No. 0.83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 0.83
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Christensen TMIE, Kragh KM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-OCT-1995 (first enry)
Alpha-1,4-glucan lyase gene.
Alpha-1,4-glucan lyase; enzyme; ss.
Morchella costata.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                   RESULT 7
Q89701/c
ID Q89701 standard; DNA; 3201 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 50.0%
.....hes 83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-APR-1995.
15-OCT-1994; E03398.
15-OCT-1993; GB-021302.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DANISCO AS.
```

S

```
The post control of the control of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tissue growth; activin; inhibin; tumour invasion suppressor; EST; human; chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis; receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
                                                                                                                                                          Morchella costata used in claimed processes of the invention. A morchella costata used in claimed processes of the invention. A claimed process of preparing a medium that contains an antioxidant and at least one other component involves preparing antioxidant from a glucan, in situ, by use of recombinant DNA techniques. Also claimed are: (1) use of anhydrofructose as an antioxidant for a medium, where the anhydrofructose is prepared in situ in the medium; (2) use of anhydrofructose for imparting or improving stress tolerance in a plant, where the anhydrofructose is prepared in situ in the plant; (3) use of glycan lyase for imparting or improving: (i) stress tolerance in plant, or (ii) transformation of grape, where the glucan lyase is prepared in situ; (4) use of a menso of inparting or improving stress tolerance in a plant, where the NS is expressed in situ in the plant, and (5) use of a NS coding for a glucan lyase for imparting or improving stress tolerance in a plant, where the NS is expressed in situ in the glucan lyase for imparting or improving the transformation of a glucan lyase for imparting or improving the transformation of a glucan lyase for imparting or improving the transformation of a grape, where the NS is expressed in situ in the grape. The antioxidant containing medium can be used as foodstuff or in the preparation of foodstuffs such as beverages, in particularly perparent or preparation of foodstuffs such as sheverages, in particularly sequence (3201 BP; 903 A; 752 C; 770 G; 776 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   968 GTATCCGCACTGATACCGTAACAATCGATACCACCATACCTGGTTCCCAGCTTGATGTAG 909°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243 ccgggcgtaaaccggtaacgcatcacctgacggaagaagaatgcaaaaagagtttcattaca 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             303 ccattggcccttattccacacccgtcctgaccatcgaacccggtgaccggattattgtcg 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1028 CIGGGCTTCAACTTTGAACGTCCAACAAGACCTGTATAAAGTCGTACAATTTCCGGGACC 969
Recombinant production of anti-oxidant compounds - by the production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D, Racie LA, Spaulding V, Treacy M; WPI: 99-070078/06. New polynucleotides encoding human secreted proteins - derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Expressed sequence tag; secreted protein; haematopoiesis regulator;
                                        an anhydrofructose from a glucan, used for improving plants for
                                                                                               Claim 9; Page 45-46; 53pp; English.
This nucleotide sequence codes for a glucan lyase (see W88255) of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         363 acactcgagatgcttttgaaggtgctatcaattcggaacaggatat 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              908 CCTGAGTTGGTCTTTCCAAAGTCGATGGCAATTTGAGAGTAGTTAT 863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.3%; Score 33.2; DB 50.0%; Pred. No. 0.83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            V88779 standard; cDNA; 383 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-OCT-1998; U06956.
10-APR-1997; US-837312.
(GEMY) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                      foodstuffs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST clone HO266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
WO9845437-A2.
                                                                         use in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          with pure alpha-1,4-glucan lyase, martic. useful as antioxidant and sweetener for foods and beverages
Claim 12, Page 101c-102b; 166pp; English.
An alpha-1,4-glucan lyase enzyme (preferably pullanase or isoamylase)
is used in a new method for the production of 1,5-D-anhydrofructose.
The enzyme is isolated from either a fungus (M.costata or M.vulgaris)
or from fungally infected algae (G.lemaneiformis) or algae alone.
1,5-D-anhydrofructose is useful as an antioxidant and sweetener for foodstuffs and beverages. It is also useful as an intermediate for the antibiotic microthecin, an oxygen scavenger during polymerisation reactions and as a reducing agent in the synthesis of blodegradable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243 ccgggcgtaaaccggtaacgcatcacctgacggaagaaatgcaaaaagagtttcattaca 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1028 CIGGGCTTCAACTTTGAACGTCCAACAAGACCTGTATAAAGTCGTACAATTTCCGGGACC 969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          303 ccattggcccttattccacacccgtcctgaccatcgaacccggtgaccggattattgtcg 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            968 GTATCCGCACTGATACCGTAACAATCGATACCATACCTGGTTCCCAGCTTGATGTAG 909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1,5-D-anhydro:fructose prodn. from alpha-1,4-glucan - by treatment
                         10-JAN-1996 (first entry)
M.costata DNA encoding alpha-1,4-glucan lyase.
Alpha-1-4-glucan lyase; 1,5-D-anhydrofructase; G.lemaneiformis; antioxidant; food additive; sweetener; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (DANI-) DANISCO AS.

Bojko M, Bojsen K, Christensen TMIE, Kragh KM, Marcussen J; Nielsen J, Yu S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               V84194;
29-MAR-1999 (first entry)
Morchella costata glucan lyase DNA.
Glucan lyase; antioxidant; transgenic plant; stress tolerance; anhydrofructose; beverage; wine; foodstuff; ds.
Morchella costata.
W09850532-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 3201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      363 acactcgagatgcttttgaaggtgctatcaattcggaacaggatat 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            908 CCTGAGTTGGTCTTTCCAAAGTCGATGGCAATTTGAGAGTAGTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              770 G;
                                                                                                                                                                                                                                                                            /*tag= a
/product= alpha_1,4_glucan_lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 33.2;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          752 C;
                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Buchter-Larsen A, Marcussen I; WPI; 99-070094/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          903 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 V84194 standard; DNA; 3201 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-OCT-1993; GB-021302.
15-OCT-1993; GB-021301.
15-OCT-1993; GB-021303.
15-OCT-1993; GB-021305.
15-OCT-1993; GB-021305.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-NOV-1998.
06-MAY-1998; IB0708.
06-MAY-1997; GB-009161.
(DANI-) DANISCO AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3201 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                     15-OCT-1994; E03397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 95-161801/21.
                                                                                                                                                                         Morchella costata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; W88255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; R70638
                                                                                                                                                                                                                                                                                                                                                  W09510616-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plastics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    V84194/c
```

a δ a ò 셤

õ

ö

0; Gaps

DB 1; Length 3201; 83; Indels

```
508 GATGGAGCTATATTTA 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                        δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                        ;
0
animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, hemanatopoiseis regulating activity, tissue growth activity, activity, activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, tumour inhibition activity. The EST sequences are also stated to be useful for gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Trans-aldolase gene - providing high level expression of trans-aldolase gene - providing high level expression of the trans-aldolase gene - providing high level expression of the therologous protein, esp. human serum albumin, in yeast, not be the subject to glucose repression.

Claim 3; Page 16; 30pp; French.

CLA: Standard ragment (05701) was isolated from a library of two lacts 2359/152 genome fragments fused to B. Coli lacz. The comprises a trong promoter sequence suitable for high level expression of recombinant proteins in Kluyveromyces or other yeast hosts. The promoter is not subject to glucose repression content yeast hosts. The promoter is not subject to glucose repression so can be used in conventional culture media. Restriction enzyment was cloned in vector pCRII to give pYG176. The KlTAL1 promoter can be removed from this plasmid by Mulr-HindIII digestion and the removed from this plasmid by Mulr-HindIII digestion and the resulting "portable promoter" is then used in the construction of vectors for expression of heterologous proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1160 ctgaacaaaaacctgttagttagtaggaataactaaccggtgaacattacccggatgta 1219
                                                                                                                                                                                                                                                                                194 CAAGGACTICTICAGCATGAAGCCGGAGTGGGAGAACTIGAACCAGTCCAACGTGCGGCG 253
                                                                                                                                                                                                                                                595 catgeteaatgateegetgeeagaaaaggtgegeatgattaaaetegaeagtgaaaaggt 654
                                                                                                                                                                                                                                                                                                                                                  254 CATGCACACGGCCGTGCGGCTGAACGAGGTCATCGTGAAGAAATCCCGGGACGCCAAGCT 313
                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         K.lactis transaldolase gene KlTAL1 portable promoter. Kluyveromyces lactis; budding yeast; transaldolase; strong promoter; portable promoter; KlTAL1; ds. Kluyveromyces lactis.
                                                                                                                                                                                                                      ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.2%; Score 32.2; DB 1; Length 1226; 63.6%; Pred. No. 0.98;
                                                                                                                                                                                       Length 383;
                                                                                                                                                                                                                     82; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                       66 T;
                                                                                                                                                                                                                                                                                                                                                                                    655 ctactggagcaaacgccatacgcttccctataaaccccatattg 698
                                                                                                                                                                                                                                                                                                                                                                                                      14 TGTTTTGCTCAACATGCCTGGGCCTCCCGGCAACGGAATGGTG 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28;
                                                                                                                                                                                      DB 1;
                                                                                                                                     117 G;
                                                                                                                                                                                    Score 32.8; DB Pred. No. 0.28; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                     108 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (RHON ) RHONE POULENC RORER SA. Bolotin M, Menart S; WPI; 94-065706/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q57702/c
ID Q57702 standard; cDNA; 1226 BP.
                                                                                                                                                                                    2.3%;
                                                                                                                                   92 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gatcggggtaatgtgta 1236
||| | | | |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-AUG-1994 (first entry)
                                                                                                                                                                                                                   82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-JUL-1993; F00771.
30-JUL-1992; FR-009432.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
'-hag 49; Conserve
                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-FEB-1994.
                                                                                                                                     Sequence
                                                                                                                    therapy
                                                                                                                                                                                                                     Matches
 88888888888
                                                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                                 임
                                                                                                                                                                                                                                                                                                                  Ω
                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                  δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    οχ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
```

```
1160 ctgaacaaaaacctgttagtttagtaggaataactaaccggtgaacattacccggatgta 1219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              640 CGGATGGACAACCGGGTAGTTTATGCGGGATGACTTTCCAGTGATCCTTGCCTGGTCGTA 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New transcriptional promoter from the Kluyveromyces lactis trans-aldoLase gene - providing high level expression of heterologous protein, esp. human serum albumin, in yeast, not subject to glucose repression claim 1; Page 14-15; 30pp; French.

A 1.3kb cDNA fragment (057701) was isolated from a library of K.lactis 2359/152 genome fragments fused to E.coli lacz. The K.lactis 2359/152 genome fragments fused to E.coli lacz. The isolated clone comprises a strong promoter sequence suitable for high level expression of recombinant proteins in Kluyveromyces or other yeast hosts. The promoter is not subject to glucose repression so can be used in conventional culture media. See also 057702. Sequence 1349 BP; 397 A; 271 C; 202 G; 479 T;
                                                                                  15.AUG-1994 (first entry)
K.lactis transaldolase gene KlTAL1 promoter.
Kluyveromyces lactis; budding yeast; transaldolase; strong promoter;
Kluyveromyces lactis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 1349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human hepatocyte nuclear factor 1 beta gene (TCF2). Human, hepatocyte nuclear factor 1 beta; HWP-1 beta; MODY4; human, transcription factor; maturity onset diabetes of the young; diabetes; NIDDM; diagnosis, therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                       /product= transaldolase_N-terminal /note= "partial CDS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.2%; Score 32.2;
63.6%; Pred. No. 1;
                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
RESULT 12
Q57701/c
ID Q57701 standard; CDNA; 1349 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                (RHON ) RHONE POULENC RORER SA. Bolotin M, Menart S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= b
/label= HNF-3
59. .69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            V52729 standard; DNA; 6260 BP.
                                                                                                                                                                                                                                        /*tag= a
1297. .1349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= NF-1
34. .46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1220 gatcggggtaatgtgta 1236
                                                                                                                                                                                                                                                                                     /*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   580 GATGGAGCTATATTTA 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-DEC-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49; Conservative
                                                                                                                                                                                                                      .1296
                                                                                                                                                                                                                                                                                                                                                 WPI; 94-065706/08.
P-PSDB; R46601.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein_bind
                                                                                                                                                                                                                    promoter
```

ô

```
Insolated nucleic acid encoding hepatocyte nuclear factor 1-alpha and 1-beta - useful for detecting susceptibility for non-insulin dependent diabetes, especially maturity-onset diabetes of the young claim 95; Fig 26A-M; 363pp; English.

This is a partial nucleotide sequence of the gene (TCF2) encoding human hepatocyte nuclear factor 1 beta (HNF-1 beta, see W71580), a homeodomain-containing transcription factor. Mutations in this gene are indicative of a propensity to diabetes mellitus. The invention concerns the identification of genes responsible for diagnostics and therapeutics. It demonstrates that the MODY3 locus
                                 /*tag= ab
/note= "n at position 3564 represents an intronic
sequence of 2 kb"
3740. .3901
                                                                                                                                                                                                                                                                                                                                                                               /*tag= aj
/note= "n at position 5177 represents an intronic
sequence of 1.5 kb"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= ao
/note= "n at position 5853 represents an intronic
sequence of 1.5 kb"
6088. .6260
                                                                                                                                                                                                                                                /*tag= ag
/note= "n at position 4339 represents an intronic
sequence of 0.8 kb"
4672. .4863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-MAR-1998.
10-SEP-1997: U16037.
10-SEP-1996: US-029679.
10-SEP-1996: US-025719.
02-00T-1996: US-028056.
(ARCH-) ARCH DEV CORP.
Bell GI, Furuta H, Horikawa Y, Kaisaki PJ, Menzel S, Oda N, Yamaqata K; PP-PSDB: W71567/24.
                                                                                       /number= 5
3902, 4018
/*tag= ad
                                                                                                                                                                                                                                                                                                  /*tag= ah
/number= 7
4864. .5326
                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= ak
/number= 8
5449. .5541
/*tag= al
/number= 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /number= 9
5687. .6087
/*tag= an
  /*tag= aa
/number= 4
3564
                                                                                                                                                                                              4221. .4671
/*tag= af
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= ap
/number= 10
                                                                                                                                                                                                                                                                                                                                                                                                                     5327. .5448
                                                                                                                                                           .4220
                                                                                                                                                                                                                        /number= 6
4339
                                                                                                                                                                                                                                                                                                                                         /*tag= ai
/number= 7
5177
                                                                                                                                                                          ae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /number= 9
                                                                                                                                             /number=
4019. .42
/*tag= a
                                                                                                                                                                                   'number=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag=
                         misc_difference
                                                                                                                                                                                                                                                                                                                                                                    misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_difference
                                                                                                                                                                                                                                     misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9811254-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        intron
                                                                                                                                                                                                 intron
                                                                                                                                                                                                                                                                                                                                intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                              intron
                                                                                                                     intron
                                                                               exon
                                                                                                                                                           exon
                                                                                                                                                                                                                                                                                                                                                                                                                        exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exon
                                                                                                                                                                                                                                                                                          exon
  /*tag= "w at position 2205 represents an intronic sequence of 3.8 kb" 2589. .2752
                                                                                                                                                                                                                                                                                                                                                                                                    / 479. .490
/ 4tag= n
/ 1abel= n
/ 1abel= HNF-3
/ 1abel= HNF-3
/ 1abel= APl
/ 15. .6215
/ 4tag= q
/ note= "contains introns"
/ 4tag= r
/ number= 1
                                               154...163...
*tag= e | /*tag= e | /*tag= f | /*tag= f | /*tag= f | /*tag= g | /*tag= g | /*tag= g | /*tag= h | /*tag= l | /*tag= l | /*tag= l | /*tag= k |
/label= AP1
113. .131
/*tag= d
/label= NF-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= x
/number= 3
2753. .3210
/*tag= Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /number= 3
3211. .3452
/*tag= z
/number= 4
3453. .3739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    041. .1756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= s
/number= 1352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_difference
             protein_bind
                                                                                                                                                                                                                                                                                   protein_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein_bind
                                                    protein_bind
                                                                                         protein_bind
                                                                                                                                protein_bind
                                                                                                                                                                      protein_bind
                                                                                                                                                                                                          protein_bind
                                                                                                                                                                                                                                                protein_bind
                                                                                                                                                                                                                                                                                                                            protein_bind
                                                                                                                                                                                                                                                                                                                                                                  protein_bind
                                                                                                                                                                                                                                                                                                                                                                                                        protein_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                               protein_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
```

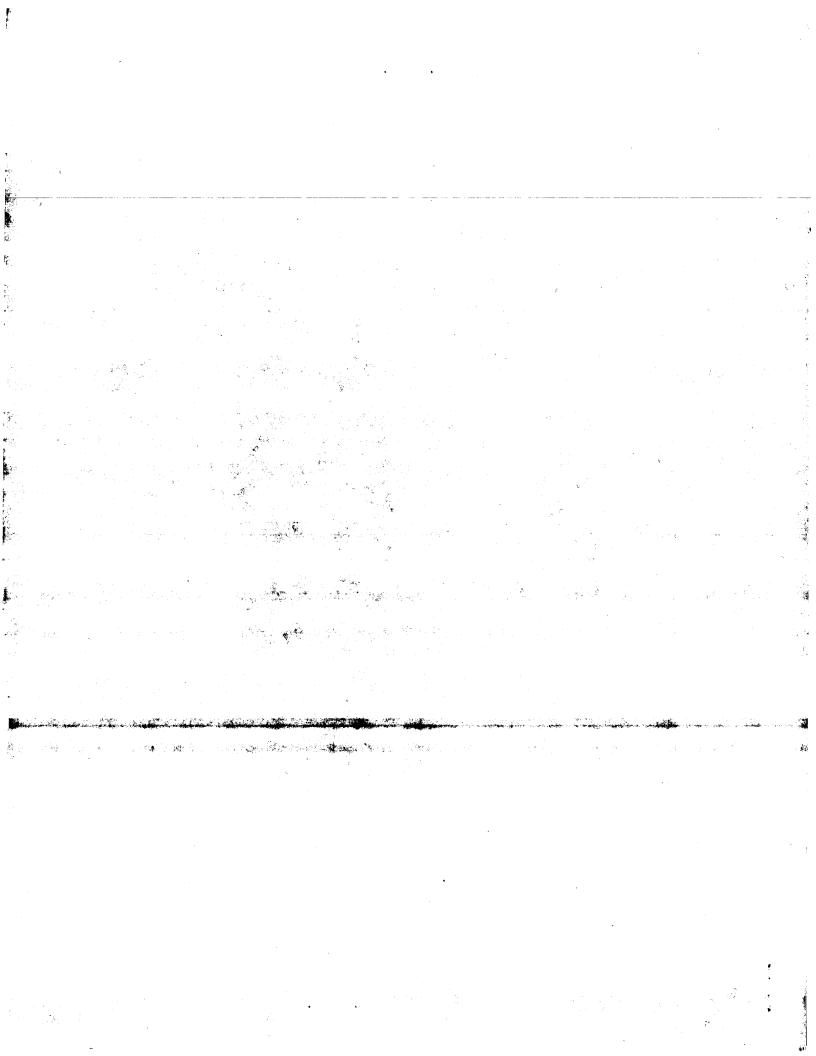
```
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                              514 gttgccccgcgcgttgatccctacggcatctgcgccatgattccgcattttggcggact 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The protein (pILSA) is capable of selectively inhibiting the cellular division of oestrogen-sensitive epithelial tumour cells and or/exerting a cytotoxic activity on such cells. It is used for treating tumours, particularly oestrogen-sensitive epithelial tumours. The protein can also be used to produce antibodies which in turn can be used in diagnostic applications.

Sequence 618 BP; 107 A; 232 C; 189 G; 90 T;
is the HNF-1 alpha gene (see V52625), the MODV4 locus is the HNF-1 beta gene (see also V52730) and the MODX1 locus is the HNF-4 alpha dene (see V52687). Analysis of mutations in these HNF genes can be diagnostic for diabetes. The invention also contemplates methods of screening for modulators of HNF function utilising HNF nucleic acids or polypeptides, the modulators being useful for treating diabetes by modulating HNF function in an animal.

Sequence 6260 BP; 1273 A; 1897 C; 1783 G; 1295 T;
                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aatccatgttgccccgcggcgttgatccctacggcatctgcgccatgattccgcattttg 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             422 ANTACACGCTGCCCCCGGTGTGGACCCCACCCAAGTTTCCTCCTCCTGTCCCTGAGG 481
                                                                                                                                                                                                                              574 gaccgggaccgacctgacggccatgctcaatgatccgctgccagaaaaggtgcgcat 630
                                                                                                                                                                                                                                           678 Gregaccegecegeceracceraraccaraccaractranacranacca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - is obtd.
                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New protein homologous to human heat shock P27 protein - is of from liposarcoma cells, used for treating oestrogen-dependent
                                                                                                                                 DB 1; Length 6260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 618;
                                                                                                                                                                                                                                                                                                                                                         Encodes protein homologous to human heat shock protein p27. Heat shock protein; tumour; oestrogen; antibodies; growth inhibition; ss.
                                                                                                                                                       53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (NAST-) IST NAZ STUDIO & CURA TUMORI FONDAZIONE. Mancini A;
                                                                                                                     Score 32.2; Di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 31.6; DB
Pred. No. 1;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         900
                                                                                                                                            Pred. No. 2.9;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gcggactgaccggaccgacctgacggccatgct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCACACTGACCGTGGAGGCCCCCATGCCCAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1997 (first entry)
P. aeruginosa detection probe #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T28490 standard; DNA; 2167 BP.
                                                                                                                             2.2%;
                                                                                                                                                                                                                                                                                                                    Q48718 standard; DNA; 618 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.2%;
                                                                                                                                                                                                                                                                                                                                            22-MAR-1994 (first entry)
                                                                                                                                                      64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    16-SEP-1993, 08-MAR-1993, IT0020. 09-MAR-1992; IT-RM0161. 30-SEP-1992; IT-RM0716.
                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93-303461/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 55; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              epithelial tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 93-303461
P-PSDB; R41022
                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
W09318147-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-APR-1997
                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                  048718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T28490;
                                                                                                                                                                                                                                                                                             RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15
                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
T28490
  888888888
                                                                                                                                                                                                      g
                                                                                                                                                                                                                               δλ
                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                  á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
```

```
ö
                                                 Staphylococcus epidermidis; Enterococcus facealis; respiratory tract; Staphylococcus saprophyticus; Streptococcus pyogenes; urinary tract; Haemophilus influenzae; Moraxella catarrhalis; septicaemia; meningitis; infection; intra-abdominal infection; skin infection; bacterial resistance; beta-lactam antibiotic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1303 attggtttactttactccttcagcggagtgacggcggcacaagagttgtcacaatggcgc 1362
            pneumonia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1363 ggagcaacccaggctattgccgaaattaatcaaaatggcggcatcaacggcagaccactc 1422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              162 ATCGGCCTGCTGTTCTCCGAAACCGGCGTCACCGCCGATATCGAGCGCTCGCACGCGTAT 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
Detection; probe; amplification primer; bacterial pathogen; pneumoni
Escherichia coli; Klebsiella pneumoniae; Pseudomonas aeruginosa;
Proteus mirabilis; Streptococcus pneumoniae; Staphylococcus aureus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        may also be used to evaluate a bacterial resistance to beta-lactam antibiotics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   222 GGCGCATTGCTCGCGGTCGAGCAACTGAACCGCGAGGGCGGCGTCGGCGGTCGCCGCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 2167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  362 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 730 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 31.2; DE Pred. No. 3.2; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               712 C;
                                                                                                                                                                                                                                                                          Roy PH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               363 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 51.4%;
Matches 72; Conservative
                                                                                                                                                                                                                                                                      Ouellette M,
                                                                                                                                                                    21-MAR-1996.
12-SEP-1995; CA0528.
12-SEP-1994; US-304732.
(BERGY) BERGERON M G.
(OUEL.) OUELLETTE M.
(ROYP/) ROY P H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2167 BP;
                                                                                                                                                                                                                                                                        Bergeron MG, Oue
WPI; 96-179953/18
                                                                                                                                                      WO9608582-A2.
                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
```

9, 2000, 21:10:56 Search completed: September Job time: 3164 sec



```
TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                               4444440000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
  υv
                                                                                                                                              ; Search time 52.2 Seconds
(without alignments)
3799.914 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 15, Appl Sequence 7, Appl Sequence 17, Appl Sequence 11, Appl Sequence 11, Appl Sequence 13, Appl Sequence 14, Appl Sequence 16, Appl Sequence 16, Appl Sequence 17, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                              1 cccgggaactccatgtggcc.....aatgcaattcatttggatcc 1442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1
Sequence 1
Sequence 1
Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/5C_COMB.seq:*
/cgn2_6/ptodata/2/ina/5C_COMB.seq:*
/cgn2_6/ptodata/2/ina/R_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-123-343A-15
US-08-123-343A-6
US-08-123-343A-6
US-08-633-770A-3
US-08-633-770A-3
US-08-633-770A-3
US-08-232-463-14
US-08-274-686-4
US-08-374-686-1
US-08-374-686-1
US-08-374-686-1
US-08-374-686-1
US-08-35-13536-2
PCT-US-95-13536-2
PCT-US-95-13536-1
US-08-825-586-45
US-08-825-586-45
US-08-825-586-45
US-08-825-586-45
US-08-825-915-6
US-08-455-107-1
US-08-452-915-6
US-08-452-915-6
US-08-452-915-6
US-08-452-915-6
US-08-452-915-6
US-08-452-915-6
US-08-452-915-6
US-08-452-915-6
US-08-452-915-6
US-08-452-915-1
US-08-452-915-6
US-08-452-915-6
US-08-452-915-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                     243080 segs, 68777915 residues
                                                                                                                                                9, 2000, 20:16:07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                               OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5268463-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5432081-1
                                                                                                                                                                                                                                                                                                                                             IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [ssued_Patents_NA:*
                                                                                                                                                                                                                                             US-09-214-679-1
1442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       length: 0
length: 1000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    503
57300
57300
77218
77218
9551
1326
1326
1187
11188
10095
265
1888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300
300
850
850
850
1212
2380
2438
                                                                                                                                                September
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30.22
30.22
30.23
30.23
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
30.33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.222223.4.
                                                                                                                                                                                                                                                Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database
                                                                                                                                                Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Š.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ပပ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    υυ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               000
```

```
Appl
Appli
Appli
Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                                                       Appl
Appl
Appl
Appl
                                                                                                                                                                                                Sequence Seq
                                                                                                                                                                                                                                                                                                                                                                     Sequence 1
Sequence 1
Sequence 2
                           Sequence
Sequence
Sequence
                                                                                                                         Sequence
Sequence
Sequence
                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Steller, Hermann
APPLICANT: Abrams, John M.
APPLICANT: Grether, Megan E.
APPLICANT: White, Kristin
TITLE OF INVENTION: Cell Death Genes of Drosophila
TITLE OF INVENTION: Melanogaster and Vertebrate Analogs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,343A
FILING DATE: 17-SEP-1993
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/004,957
FILING DATE: 15-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/POCKET NUMBER: 32,227
REFERENCE/COMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
US-08-452-267-2
US-08-723-624-18
US-08-723-624-19
US-08-723-624-19
US-08-525-507-14
US-08-817-188-5
US-08-817-188-5
US-08-818-772A-2
US-08-818-772A-2
US-08-819-86-2
US-08-819-86-2
US-08-819-86-2
US-08-819-86-2
US-08-819-86-2
US-08-920-812-13
US-08-920-812-13
US-08-920-812-13
US-08-920-812-13
                                                                                                                                                                                                                                                                                                                                         US-08-362-577C-13
US-08-920-828-13
US-09-092-025A-1
                                                                                                                                                                                                                                                                                                                                                                                                                US-08-361-708-2
US-08-536-277-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 15, Application US/08123343A Patent No. 5593879 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 503 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
     2633
3035
31035
3105
3105
3105
5560
5560
7742
118986
118986
118986
9515
9515
9515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown
  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-123-343A-15/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 02173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-123-343A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
  000000
```

DB 1; Length 503;

2.6%; Score 37.6;

7

```
380 gaaggtgctatcaattcggaacaggatattccgagccagttgctaaaaatgccctttctc
                                                                                                                      1398 GGAGCTCTTCTTCCGGGGGGGGGATGCGTCCATTGAACTCCTGCAGACGCTCCGGGC
                                                                                                                                                                          440 aacccacaaaacggaccgatcatggtcaatggcgcggagaaaggtgatgctcgctgtc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Megrowitz, Elliot M.
APPLICANT: Clark, Steven E.
APPLICANT: Clark, Steven E.
APPLICANT: Williams, Robert W.
TITLE OF INVENTION: Plant Clavatal Nucleic Acids,
TITLE OF INVENTION: Transformed Plants, and Proteins
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUWRRY: United States
ZIP: 94111-4187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,553A
FILING DATE: 06-JUN 1995
CLASSIFICATION: 800
ATTONREY/AGENT INFORMATION:
NAME: SILVA, RObin M.
REGISTRATION NUMBER: 38,304
REGISTRATION NUMBER: 38,304
REGISTRATION NUMBER: MADER: A-60086/RFT/RMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 34.2; DB 3;
Pred. No. 0.56;
0; Mismatches 83;
                                                                                                                                                                                                                                                                                                                      1278 GTACTCGCGCTCATCCTCGCCCGTCGAGGTCA 1247
                                                                                                                                                                                                                                                                       500 tatatogaatccatgttgccccgcggcgttga 531
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08473553A
Patent No. 5859338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELERAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5733 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 2.4
Best Local Similarity 50.3
Matches 84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5117..5467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: unkno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-473-553A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-473-553A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGIH:
                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                          δy
                                  ö
                                                                  320 acaccogtcctgaccatcgaacccggtgaccggattattgtcgacactcgagatgctttt 379
                                                                                                            334 ACCACCGGACTGGCTGTCGGTATGCAGAGTGGATTATTGCTGCTGCTGCTGCTATT 275
                                                                                                                                                             380 gaaggtgetatcaattcggaacaggatattccgagccagttgctaaaaatgccetttctc 439
                                                                                                                                                                                                          274 GGAGCTCTTCTTCCTGGGGGGGGATGCGTCCATTGAACTCCTGCAGACGCTCCCGGCC 215
                                                                                                                                                                                                                                                           440 aacccacaaaacggaccgatcatggtcaatggcgcggagaaaggtgatgtgctcgctgtc 499
                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       320 acacccgtcctgaccatcgaacccggtgaccggattattgtcgacactcgagatgctttt 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 37.6; DB 1; Length 3900;
Pred. No. 0.032;
0; Mismatches 109; Indels 0
  Pred. No. 0.0091;
0; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Steller, Hermann
APPLICANT: Abrams, John M.
APPLICANT: Grether, Megan E.
APPLICANT: Grether, Megan E.
APPLICANT: Grether, Melan E.
APPLICANT: Grether, Melan E.
APPLICANT: Grether, Melan E.
TITLE OF INVENTION: Cell Death Genes of Drosophila
TITLE OF INVENTION: Melanogaster and Vertebrate Analogs NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,343A
FILING DATE: 17-SEP-1993
CLASSIFCATION: 800
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/004,957
FILING DATE: 15-Jan-1993
ATTORNEY AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REGISTRATION NUMBER: 32,227
REGISTRATION NUMBER: 32,227
                                                                                                                                                                                                                                                                                                                                                                                      154 GTACTCGCGCTCATCCTCGCCCGTCGAGGTCA 123
                                                                                                                                                                                                                                                                                                                                                      500 tatatogaatocatgttgccccgcggcgttga 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: MIT-5907A TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEPAX: 61861-9540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-123-343A-6/c

Sequence 6, Application US/08123343A

Patent No. 5593879

GENERAL INFORMATION:

APPLICANT: Steller, Hermann
Best Local Similarity 48.6%;
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 2.6%;
Best Local Similarity 48.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 3900 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: CDNA
US-08-123-343A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 02173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
                                                                                                                                                                ò
                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                     QQ
                                                                                                                                                                                                                                                        QY
                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
```

```
ô
  Gaps
ó
  δ
```

Length 5733;

```
APPLICANT: Bojsen, Kirsten
APPLICANT: Yu, Shukun
APPLICANT: Kragh, Karsten
APPLICANT: Kragh, Karsten
APPLICANT: Christensen, Tove
APPLICANT: Marcussen, Jan
TITLE OF INVENTION: ALPHA-1,4-GLUCAN LYASE FROM A FUNGUS, ITS
TITLE OF INVENTION: PURIFICATION GENE CLONING AND EXPRESSION IN MICROORGANISMS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1681 GTATCCGCACTGATACCGTAACAATCGATACCAGTACCTGGTTCCCAGCTTGATGTAG 1622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1741 CTGGGCTTCAACTTTGAACGTCCAACAAGACCTGTATAAAGTCGTACAATTTCCGGGACC 1682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      303 coattggcccttattccacacccgtcctgaccatcgaacccggtgaccggattattgtcg 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243 ccgggcgtaaaccggtaacgcatcacctgacggaagaaatgcaaaaagagtttcattaca 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PATENTIN STATEM.

SOFTWARE: PATENTIN DATA:

CURRENT APPLICATION DATA:

**APPLICATION NUMBER: US/08/633,770A

FILING DATE: Unly 8, 1996

CLASSIFICATION DATA:

APPLICATION UNMBER: PCT/EP94/03398

FILING DATE: OCT-15-1994

ATTONER; ACTENT INDEMATION:

NAME: Altumn, Daniel E

REGISTRATION NUMBER: 24,115

REGISTRATION NUMBER: 34,115

REGISTRATION UNBER: A115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                363 acactcgagatgcttttgaaggtgctatcaattcggaacaggatat 408
  363 acactcgagatgcttttgaaggtgctatcaattcggaacaggatat 408
                                               908 CCTGAGTTGGTCTTTCCAAAGTCGATGGCAATTTGAGAGTAGTTAT 863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 33.2; DB 3;
Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                 Sequence 11, Application US/08633770A Patent No. 5908760 GENERAL INFORMATION: APPLICANT: Bojsen, Kirsten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: DY TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 4726 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 2.3°
Best Local Similarity 50.0°
Matches 83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 714-760-9502
TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE:
US-08-633-770A-11
                                                                                                                       RESULT 5
US-08-633-770A-11/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŏ
    ò
                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:

APPLICANT: Bojsen, Kirsten

APPLICANT: Yu, Shukun

APPLICANT: Kragh, Karsten

APPLICANT: Kragh, Karsten

APPLICANT: Marcussen, Jan

APPLICANT: Marcussen, Jan

TITLE OF INVENTION: ALPHA-1,4-GLUCAN LYASE FROM A FUNGUS, ITS

TITLE OF INVENTION: PURIFICATION GENE CLONING AND EXPRESSION IN MICROORGANISMS

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
1196 accggtgaacattacccggatgtagatcggggtaatgtgtaagttcaaacaatcgctatt 1255
                                                                                         3769 ACTGATAATITCTICTCCGGTGAACTICCGGTAACGATGTCCGGCGATGTTCTCGATCAG 3828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    303 ccattggcccttattccacacccgtcctgaccatcgaacccggtgaccggattattgtcg 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               243 ccgggcgtaaaccggtaacgcatcacctgacggaagaaatgcaaaaagagtttcattaca 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1028 CTGGGCTTCAACTTTGAACGTCCAACAAGACCTGTATAAAGTCGTACAATTTCCGGGACC 969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 33.2; DB 3; Length 3201;
Pred. No. 0.84;
0; Mismatches 83; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATURG SYSTEM: DOS
SOFFWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/633,770A
FILING DATE: July 8, 1996
CLASSIFICATION: 435
PRICA PLICATION DATA:
APPLICATION NUMBER: PCT/EP94/03398
FILING DATE: OCT-15-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                   3829 ATTTACCTCTCTAACAACTGGTTTTCCGGCGAGATTCCACCTGCGAT 3875
                                                                                                                                           1256 tttaacagctaaagcaggtgcatatggggccagatacacccatcaat 1302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUDRESSEE: Knobbe, Martens, Olson & Bear
STRRET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: DYOUG.001APC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08633770A Patent No. 5908760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic) US-08-633-770A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 2.3%;
Best Local Similarity 50.0%;
Matches 83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 3201 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U.S.A.
                                                                                                                                                                                                                                                                  RESULT 4
US-08-633-770A-3/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                           g
```

```
1351 tcacaatggcgggagcaacccaggctattgccgaaattaatcaaaatggcggcatcaac 1410
                              3064 CGAGAGCGCCAAGACAGAGTGTTCCAGGAGGAAGAAGAAGAAGAGGAGGAGGAGGAG 3123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 cgggaactccatgtggccgtgatcctggtcgagcaggatattgcgatgatccagcgggcc 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Steinert, Peter M.
APPLICANT: Lee, Seung-Chul
APPLICANT: Kim, In-Gyu
APPLICANT: Kim, In-Gyu
APPLICANT: Kim, In-Gyu
APPLICANT: Chung, Sco-11
APPLICANT: Park, Sang-Chul
ITLE OF INVENTION: Trichohyalin and Transglutaminase-3 and
TITLE OF INVENTION: Mehods of Using Same
NUMBER OF SEQUENCES: 117
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: GLO Newport Center Drive, Sixteenth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.2%; Score 32.4; DB 1; 50.0%; Pred. No. 3.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Fedrick, Michael F.
REGISTRATION NUMBER: 36,799
REFERENCE/DOCKET NUMBER: NIH054.001A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (714),760-0404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/056,200 FILING DATE: 30-APR-1993 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PC-DOS/MS-DOS
                                                                                                                                                                                                                                  Sequence 93, Application US/08056200 Patent No. 5616500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (714) 760-0404
TELEFAX: (714) 760-9502
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 9551 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 2.27
Best Local Similarity 50.07
Matches 81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 620 Newport
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
2512..8070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1507..1644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGI.

MOLECULE TYPE: CD
                                                                                  1411 ggcaga 1416
                                                                                                                1092 RRRRRR 1087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                          US-08-056-200-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
US-08-056-200-93
                                         g
                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1051 ggtagaagactttggcttcgaacaatgggatgcctacatgcttctgagtcaatgcggcaa 1110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1111 agtgcggctgggcaacatggtcgaccccaaatacaccgttggcgcgatgctgaacaaaa 1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1171 cctgttagtttagtaggaataactaaccggtgaacattacccggatgtagatcgggggtaa 1230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1231 tgtgtaagttcaaacaatcgctatttttaacagctaaagcaggtgcatatggggccagat 1290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acacccatcaatattggtttactttactccttcagcggagtgacggcggcacaagagttg 1350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 7218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 2.3%; Score 32.8; DB 1;
Best Local Similarity 3.6%; Pred. No. 1.9;
Matches 13; Conservative 193; Mismatches 160;
                                                   GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOMLPOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 30472/114 IMMU TELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300
                                                                                                                                                                                                      SEEE: Foley & Lardner
:: 1800 Diagonal Road, Suite 500
Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
               Sequence 14, Application US/08232463 Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 26-AGG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,7
                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
EDNESS: single
                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 22313-0299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX:
                                                                                                                                                                                                                          STREET:
```

δ g δ q δy g δλ g ò g

S

```
1160 ctgaacaaaaacctgttagttagtaggaataactaaccggtgaacattacccggatgta 1219
                                    3064 CGAGAGCGCCAAGACAGAGTGTTCCAGGAGGAAGAAGAAGAAGGAGGAAGCGCGAG 3123
                                                                                                              3 cgggaactccatgtggccgtgatcctggtcgagcaggatattgcgatgatccagcgggcc 62
                                                                            63 gcacagogotgtgcggtaatggataaaggcotggttgtagaaacgotgacccaacaacag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1226;
                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: K. Lactis Transaldolase Gene Promoter TITLE OF INVENTION: and Use Thereof NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                           123 ctctctgatgatcttttaatgcgtcgtcatctggctctgtaa 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/OB/374,686
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.2%; Score 32.2; DB 1;
63.6%; Pred. No. 0.99;
tive 0; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/FR93/00771
FILING DATE: 28-JUL-1993

PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: FR 92/09432
FILING DATE: 30-JUL-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 500 Arcola Rd. 3C43
CITY: Collegeville
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                               RESULT 9
US-08-374-686-4/C
Sequence 4, Application US/08374686
Patent No. 5616474
GENERAL INFORMATION:
APPLICANT: Bolotin, Monique
APPLICANT: Menart, Sandrine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Smith, Julie K.
REGISTRATION NUMBER: 38,619
REFERENCE/DOCKET NUMBER: STG
TELECOMMUNICATION:
TELEPHONE: (610)454-3839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (610)454-3839
TELEFAX: (610)454-3808
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1226 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1220 gatcggggtaatgtgta 1236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 63.69
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 19002
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: 11; MOLECULE TYPE: ; ANTI-SENSE: NO US-08-374-686-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ద
                                    Q
                                                                            δ
                                                                                                          g
                                                                                                                                                    ò
                                                                                                                                                                                         q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                        63 gcacagcgctgtgcggtaatggataaaggcctggttgtagaaacgctgacccaacaacag 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 32.4; DB 4; Length 9551; Pred. No. 3.1; 0; Mismatches 81; Indels 0
                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Trichohyalin and Transglutaminase-3 and TITLE OF INVENTION: Mehods of Using Same NUMBER OF SEQUENCE: 117 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.

ZIP: 92660
COMPUTER READABLE FORM:
MEDIOW TYPE: FLOPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,644
FILING DATE: 14-FEB.1997
CLASSIFICATION: 4.24
                                                                                                ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
CITY: Newport Beach
                                                                          123 ctctctgatgatcttttaatgcgtcgtcatctggctctgtaa 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Fedrick, Michael F.
REGISTRATION NUMBER: 36,799
REFERENCE/DOCKET NUMBER: NHU54.001A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/056,200
FILING DATE: 30-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                       RESULT 8
US-08-800-644-93
; Sequence 93, Application US/08800644
; Patent No. 5958752...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (714) 760-0404
TELEFAX: (714) 760-9502
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
LENGTH: 9551 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Steinert, Peter M. APPLICANT: Lee, Seung-Chul APPLICANT: Kim, In-Gyu APPLICANT: Chung, Soo-Il APPLICANT: Park, Sang-Chul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
2512..8070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             intron
1645..2511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: CDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 81; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: NO FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY:
; LOCATION:
US-08-800-644-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                  αq
                                                                                                            Ω
  ò
                                                                          δ
```

셤

```
APPLICANT: BERGERON, Michel G.
APPLICANT: BERGERON, Francois J.
APPLICANT: PICARD, Francois J.
APPLICANT: OUELLETE, Marc
APPLICANT: ROY, Paul H.
TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: QUARLES & BRADY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1303 attggtttactttactccttcagcggagtgacggcggcacaagagttgtcacaatggcgc 1362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1363 ggagcaacccaggctattgccgaaattaatcaaaatggcggcatcaacggcagaccactc 1422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                222 GGCGCATTGCTCGCGGTCGAACTGAACCGCGAGGGGGGCGCGTCGGCGCGCCGATC 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 2167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                CUDNIME: USA

CUDNIME: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,637B
FILING DATE: 04-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/56,840
FILING DATE: 11.5EP-1995
ATORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.
REGISTRATION NUMBER: 85.433
REFERENCE/DOCKET NUMBER: 85.543
REFERENCE/DOCKET NUMBER: 85.543
REFERENCE/DOCKET NUMBER: 85.543
REFERENCE/DOCKET NUMBER: 377-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.2%; Score 31.2; D
Best Local Similarity 51.4%; Pred. No. 3;
Matches 72; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                             ADDRESSEE: QUARLES & BRADY
STREET: 411 EAST WISCONSIN AVENUE
CITY: MILWAUKEE
             Sequence 16, Application US/08743637B Patent No. 5994066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Pseudomonas aeruginosa
US-08-743-6378-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 16, Application US/08526840B
Patent No. 6001564
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1423 aatgcaattcatttggatcc 1442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               282 GAAACGCTGTCCCAGGACCC 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 2167 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (414) 277-50
TELEFAX: (414)277-5591
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid
                                                                                                                                                                                                                                                                                                                                                                    WISCONSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
US-08-526-840B-16
                                                                                                                                                                                                                                                                                                                                                               STATE: W
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1160 ctgaacaaaacctgttagtttagtaggaataactaaccggtgaacattacccggatgta 1219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.2%; Score 32.2; DB 1; Length 1349; 63.6%; Pred. No. 1.1; tive 0; Mismatches 28; Indels 0
                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Bolotin, Monique
APPLICANT: Bolotin, Monique
APPLICANT: Menart, Sandrine
TITLE OF INVENTION: K. lactis Transaldolase Gene Promoter
TITLE OF INVENTION: and Use Thereof
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 19002
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/374,686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR93/00771
FILING DATE: 28-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/09432
FILING DATE: 30-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Julie K.
REGISTRATION NUMBER: 38,619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: ST92048-US TELECOMMUNICATION INFORMATION: TELEPHONE: (610)454-3839
TELEFAX: (610)454-3808
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 1349 base pairs
                                                                                                                                                                                                                                                                                                               : Rhone-Poulenc Rorer Inc.
500 Arcola Rd. 3C43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Kluyveromyces lactis
                                                                                                            Sequence 1, Application US/08374686
Patent No. 5616474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1220 gatcggggtaatgtgta 1236
508 GATGGAGCTATATTTA 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      580 GATGGAGCTATATTTA 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 63.6
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
1297..1347
                                                                                                                                                                                                                                                                                                                      STREET: 500 cr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: NO
ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                       US-08-374-686-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
LOCATION:
US-08-374-686-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
```

ö

RESULT 11

δy g ò

```
822 ctggaggccgcctgtttattggtgatgcccatgcttgtcagggtgatggtgagatttgcg 881.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            868 CTGAATCTGGCCTGCGTGTTGGTGCAGATATCTCTGTGGGGGCTATGATGATACTGAAG 927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 6; Length 1187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: SKOPEK, THOMAS R
TITLE OF INTENTION: SYNTHESIS OF METHYLASE RESISTANT GENES
NUMBER OF SEQUENCE: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 928 ACAGCTCATGITATATCCCACCAAGCACCACCATCAAACAGGATT 973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           882 ggaccgcagtagagtttgcctcaatcaccatcaaagtcgattt 927
                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US95/13536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Box 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 30.8; DB
Pred. No. 2.9;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: ELLIOTT KORSEN
STREET: 126 E. Lincoln Avenue, P.O.
CITY: Rahway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: KORSEN, ELLIOTT
REGISTRATION NUMBER: 32,705
REFERENCE/DOCKET NUMBER: 19257Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application PC/TUS9513536
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: KORSEN, ELLIOTT
REGISTRATION NUMBER: 32,705
REFERENCE/DOCKET NUMBER: 19257
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-5493
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1187 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.1%;
                                                                                                                                                                                                                                                                                                              13-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 55.77
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 1 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S
                                                          Rahway
                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07065
                                                                                                                         07065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCT-US95-13536-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT-US95-13536-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
APPLICANT: OUELLETTE, Marc
APPLICANT: OUELLETTE, Marc
APPLICANT: ROY, Paul H
TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND
TITLE OF INVENTION: COMMON BACTERIAL PATHOGENS AND ANTIBLOTIC RESISTANCE GENES
TITLE OF INVENTION: COMMON BACTERIAL PATHOGENS AND ANTIBLOTIC RESISTANCE GENES
TITLE OF INVENTION: FOR CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
CORRESPONDENCE ADDRESS:
ADDRESSE: QUARLES & MANNO
STREEP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1303 attggtttactttactccttcagcgggagtgacggcggcacaagagttgtcacaatggcgc 1362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1363 ggagcaacccaggctattgccgaaattaatcaaaatggcggcatcaacggcagaccactc 1422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162 ATCGGCCTGCTGTTCTCCGAAACCGGCGTCACCGCCGATATCGAGCGCTCGCACGCGTAT 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                222 GGCGCATTGCTCGCGGTCGAGCAACTGAACCGCGAGGGCGGCGTCGGCGGTCGCCCGATC 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 2.2%; Score 31.2; DB 5; Length 2167; Best Local Similarity 51.4%; Pred. No. 3; Matches 72; Conservative 0; Mismatches 68; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application PC/TUS9513536
GENERAL INFORMATION:
APPLICANT: SKOPEK, THOMAS R
TITLE OF INVENTION: SYNTHESIS OF METHYLASE RESISTANT GENES
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: ELLIOTT KORSEN
                                                                                                                                                                                                                                                                                                                               STATE: Wisconsin
COUNTRY: USA
ZIP: 53202-4497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/526,840B
FILING DATE: 11-SEP-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 126 E. Lincoln Avenue, P.O. Box 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35,433
ER: 850586.90012
                                                                                                                                                                                                                                                               E: QUARLES & BRADY
411 East Wisconsin Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/304,732
FILING DATE: 12-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Pseudomonas aeruginosa
US-08-526-840B-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: BAKER, Jean C.
REGISTATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 8505E
TELECOMMUNICATION INFORMATION:
TELEFAX: (414) 277-550
TELEFAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS:
LENGTH: 2167 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1423 aatgcaattcatttggatcc 1442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         282 GAAACGCTGTCCCAGGACCC 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                Milwaukee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCT-US95-13536-2
                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
```

οy

g ò

ò

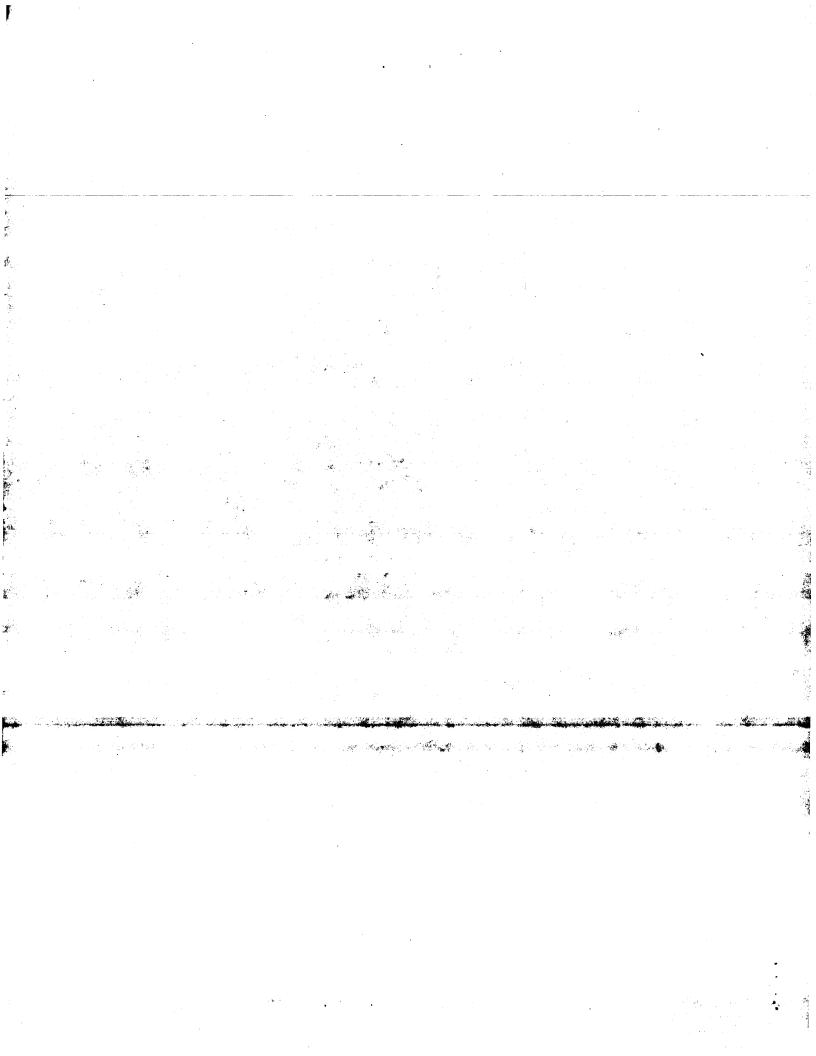
ö

```
822 ctggaggccgcctgtttattggtgatgcccatgcttgtcagggtgatggtgagatttgcg 881
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
2.1%; Score 30.8; DB 6; Length 1188;
Best Local Similarity 55.7%; Pred. No. 2.9;
Matches 59; Conservative 0; Mismatches 47; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 45, Application US/08822586
Patent No. 6015890
GENERAL INFORMATION:
APPLICANT: WILLIAM R. JACOBS, JR., JAMES M. MUSSER AND
APPLICANT: AMALIO TELENTI
TITLE OF INVENTION: AN EMBCAB OPERON OF MYCOBACTERIA AND
TITLE OF INVENTION: MUTANTS THEREOF
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          882 ggaccgcagtagagtttgcctcaatcaccaccatcaaagtcgattt 927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        928 ACAGCTCATGTTATATCCCACCACCACCACCATCAAACAGGATTT 973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READALE FORM:
MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE
MEDIUM TYPE: DISKETTE
COMPUTER: IBM CCOMPATIBLE
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,586
FILING DATE: MARCH 20, 1997
ATTORNEY/AGENT INFORMATION:
NAME: ELIZABETH A. BGGOSIAN
REGISTRATION NUMBER: 95/911
REBERBENCE/DOCKET NUMBER: 96700/437
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 100-581-4766
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: AMSTER, ROTHSTEIN & EBENSTEIN STREET: 90 PARK AVENUE CITY: NEW YORK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-5493
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1188 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genomic DNA
                                                                                                                                                                                                                                                                                    internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: NEW YORK COUNTRY: U.S.A. ZIP: 10016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: lin
; MOLECULE TYPE:
; HYPOTHETICAL: N
US-08-822-586-45
                                                                                                                                                                                                                                                                             ; FRAGMENT TYPE:
PCT-US95-13536-1
                                                                                                                                                                                                                                                            ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-822-586-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
```

```
ö
                                                                                                                                                              961 ggagaatgccgaaaatattatgagtattggcagtgcacgtccgctggaggatgcgacgcg 1020
                                                                                                                  2958 CCCGAGCACCCCACCCAGGTCCGGTTGGTCGCCCACCAGGATCTGGCGCCAGCA 3017
                                                                                                                                                                                                       3018 CTGGATCGCCTCACACCACCACGCGGATTCCGCGGGGTGCGCACGCTGCAGAACGTGGG 3077
                                                                                901 ctcaatcaccatcaaagtcgatttgatcaagaactggcagctttcctggccacgaat 960
                                                 Gaps
                                                 ö
Score 30.2; DB 5; Length 10095; Pred. No. 17; 0; Mismatches 78; Indels 0;
                                                                                                                                                                                                                                                1021 aattgcatatcgcgacttaatttactggctggtag 1055
                                                                                                                                                                                                                                                                              3078 CGCAGCGGATCCGGTCTTCCTGGACTGGCTGGTGG 3112
  2.18;
                     Best_Local Similarity 49.79
Matches 77; Conservative
  Query Match
                                                                                    δ
                                                                                                                                                                ά
                                                                                                                                                                                                         q
                                                                                                                                                                                                                                                  δλ
```

Search completed: September 9, 2000, 20:47:22 Job time: 1875 sec

ö



```
em_gss12:*
gb_gss12:*
                                                                                          em_est23:..
em_est25:..
em_est25:..
em_est25:..
em_est26:..
gb_est33:..
gb_est33:..
gb_est36:..
gb_est36:..
gb_est36:..
gb_est36:..
gb_est47:..
gb_est47:..
gb_est47:..
gb_est47:..
gb_est48:..
em_est32:..
gb_est46:..
gb_est51:..
gb_est51:..
gb_est51:..
gb_est52:..
gb_est53:..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                em_gss4:*
gb_gss5:*
9D_est25:*
9D_est26:*
9D_est28:*
9D_est29:*
9D_est30:*
9D_est31:*
9D_est31:*
9D_est31:*
9D_est21:*
em_est21:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        em_gss11:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              em_gss10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gb_gss10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4:7ssg_dg
; Search time 588.37 Seconds (without alignments) 10807.778 Million cell updates/sec
                                                                                                          1 cccgggaactccatgtggcc.....aatgcaattcatttggatcc 1442
                                                                                                                                                                     10495684
       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                   5247842 segs, 2204914090 residues
                                                        9, 2000, 20:02:07
                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                       OM nucleic - nucleic search, using sw model
                                                                                                                          IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                         US-09-214-679-1
1442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gb_est14:*
gb_est15:*
gb_est16:*
gb_est17:*
gb_est18:*
gb_est18:*
                                                                                                                                                                                                                                                                                                                                  em_est10:*
em_est11:*
                                                                                                                                                                                                                                                                                                                                                                                    em_est16:*
em_est17:*
em_est18:*
em_est19:*
gb_est1:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                               gb_est6:*
gb_est7:*
gb_est8:*
gb_est9:*
gb_est10:*
gb_est11:*
                                                                                                                                                                                                                                                                                                                                                   em_est12:*
em_est13:*
em_est14:*
em_est15:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gb_est12:*
gb_est13:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gb_est21:*
gb_est22:*
gb_est23:*
gb_est24:*
                                                                                                                                                                                                                                                                                                                                                                                                                              gb_est2:*
gb_est4:*
gb_est5:*
                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 1000000
                                                                                                                                                                                                                                                       em_est1::
em_est2::
em_est3::
em_est4::
em_est5::
em_est7::
em_est8::
em_est8::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gb_est20
                                                         September
                                                                                                                                                                                                                                                EST:*
                                                                                         Title:
Perfect score:
                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                Database :
                                                                                                           Sequence:
                                                                                                                                                    Searched:
                                                         Run on:
```

~

```
9b-9ss14:*
9b-9ss15:*
9b-9ss16:*
9b-9ss17:*
9b-9ss18:*
  gb_gss13:*
                                                em_gss13:*
117:
118:
119:
120:
121:
122:
123:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		фP				
Result No.	Score	Query	Length	DB		iption
	6	,	;	71	AW380638	RC2-HT
7	9	٠	1101	122	ເກ	L064465 Drosoph
о Э	35	2.4	268	20	733	733 ze63b1
	35	•	421	86	33	05£04
S S	32	2.4	441	20	AA019639	3639 ze62g01.
	32	2.4	492	20	Š	1557 ze46d06
	m,	2.4	691	120		51 CIT-HSP-2
	4	2.4	396	105	3	392 HS_51
,	4	2.4	422	104	526	559
	4	2.4	475	43	7	570 wq41e0
c 11	34.8	2.4	477	38		357 qp53e12.
	4	2.4	502	37	12	76 gw12a01.
Η,	4	2.4	511	103	AQ482699	8699 RPCI-11
c 14	4		562	103	96	AQ478968 RPCI-11-2
_	4	2.4	483	31	2	AA833827 od62c06.s
16	4	•	491	82	н08687	H08687 y193e12.rl
c 17	4	2.4	623	120	B69197	B69197 CIT-HSP-205
٦	4		1100	122	CNSOODYG	AL077401 Drosophil
c 19	34	•	347	88		51 yi
20	m ,	•	565	102	8	AQ430850 HS_5103_A
~ (	٠ س		352	36	4	AI216944 SWOVAFCAP
C 22	m e	•	481	21	AA084699	1699 zn05d08
~ (	· ·	•	933	114	9	)661 HS_5574
~ (	m (		352	72	N.	474829 xy07a05
~ ~	n.	•	334	82	ноз706	42g10.
0 20	33.4		384	68		3420 ya88h06.s
7 (	n	•	503	20	m,	zf57a06.
7 (	7	•	1011	123	CNS016T7	3 Drosoph
7 (			385	26	542	zw48e12
יי רי	ή·		398	25	- 1	04h12
י ר			477	200	7,5	xc51d01.
2 6			423	2 0		ob32b02.
י ר	•		477	א נ ע	200	ag43e05.
0 0			174	<b>^</b> 0	404	qo55b05.
ינ	•		0.0	ם כ	77/	1/126 qp55d12.
י נ	•		401	77	0000	50583 zo69eU7.
<b>^</b> (	· .		401	n n	7790	56118 qy52e05.
<b>7</b> ) (7)	ή,		491	35	1298	2989 oz70c0
. O	'n.		492	20	01630	02 ze38d0
4	'n.		497	36	15105	1059 qb6
c 41	m.		497	42	5911	69110 wb8
4	ς.		512	32	91827	1827
4	œ.		515	35	07439	74392 oq98d02.
	۳.		551	33	04	29044 on50b02.
4	ς.		552	63	950	9508 xd19f1

### ALIGNMENTS

AW380638 280 bp mRNA EST 04-FEB-2000 RC2-HT0275-011199-011-f11 HT0275 Homo sapiens CDNA, mRNA sequence. AW380638 RESULT 1
AW380638
LOCUS
DEFINITION ACCESSION

.

AUTHORS TITLE

REFERENCE

Tel: +55-11-2704922
Fax: +55-11-270001
Email: sainpsondeludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC2&t2=RC2-HT0275-011199-011-fl1&t3=1999-11-01&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 37
High quality sequence stop: 111.
Location/Qualifiers
1. 280
//organism="Homo sapiens"
//organism="Homo sapiens"
//organism="Homo sapiens"
//dev stage="Adult"
//dev stage="Adult" /note="Organ: head\_neck; Vector: puc18; Site\_1: Smal; Site\_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions. ö Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 280)
HCGP http://www.ludwig.org.br/ORESTES.
HCGP http://www.ludwig.org.br/ORESTES.
The FARESPLICK Human Cancer Genome Project
Unpublished (1999)
On Jul 7, 1999 this sequence version replaced gi:5866454.
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, CNS0037Q 1101 bp DNA GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR08K14 of RPCI-98 library from Drosophila melanogaster (fruit Gaps Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Metazoa; Arthropoda; Tracheata; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (Dases 1 to 1101)
Genoscope.
Direct Submission ö 2.7%; Score 39.6; DB 71; Length 280; llarity 63.8%; Pred. No. 0.12; Conservative 0; Mismatches 34; Indels 0. 567 geggaetgaeegggaeeggaeeggeeatget 600 143 GCACACTGACCGTGGAGGCCCCCAGGCCCCAAGCT 176 fly), genomic survey sequence. AW380638.1 GI:6885297 AL064465.1 GI:4941722 1101 bp Similarity fruit fly. CNS00370 9 Query Match Best Local Simi Matches 60; source LOCUS ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT ORGANISM BASE COUNT KEYWORDS SOURCE RESULT 2 CNS0037Q ACCESSION VERSION KEYWORDS SOURCE FEATURES VERSION ORIGIN g δ g

m

Page

```
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                          and Marra, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97044478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Sim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                             TITLE
JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 4
H75593/c
                                                                                                                           AUTHORS
                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutovyo Osogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; no bw sp. the same strain used for the BDGP's and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://www.inch.id.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA020733 268 bp mRNA EST 30-JAN-1997
EST 30-JA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     993 GWVCVBNWKVKMGNKMKMGMVTVNGMKMBMBVNNMKVNMKWKMGRTNKRTMKMGHTHGW 1052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            246 ggcgtaaaccggtaacgcatcacctgacggaagaaatgcaaaaaagagtttcattacacca 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           813 KRGAMKVMKADAMRRARHWARWANGAGHNTVNNVBVNMGNGMKSKGMGNTKNKVNSVKT 872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   366 ctcgagatgcttttgaaggtgctatcaattcggaacaggatattccgagccagttgctaa 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          873 VKBHKDHKTTTTTTTTTNTNMNTHTTHVMBMBMGMGMRMDMGMGRGVVGHRVGKMNGMNRMM 932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      426 aaatgccctttctcaacccacaaaacggaccgatcatggtcaatggcgcggagaaaggtg 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             486 atgtgetegetgtetatategaateeatgttgeeeegeggegttgateeetaeggeatet 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     186 gagaataacatatgaaatggttggaagaatccattatggccaaacgcggtgttggtgccg 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                693 KWGRVWBDNVKAATTDTMTKTRMAVAMARAGAAMARTAMRARAAAKAARAKKANKKKGTK 752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                753 ATKDKMGMKMGWKHKKKKDMKMDGAKATAWAMTRAGAVGAKARRAMKATRWAGAARRVKA 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           306 ttggcccttattccacacccgtcctgaccatcgaacccggtgaccggattattgtcgaca 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 933 VMRMVNWYKVKAVAVMGMMWWMMWMGAMVMWMMMGMGYSGSGSKVSCKGSTWGKKNGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              459 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                546 gegecatgatteegeattttggeggaetgaeegggaeegaeet 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 2.5%; Score 36.2; DB 122;
1 Similarity 12.2%; Pred. No. 2.4;
49; Conservative 173; Mismatches 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              129 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="BACR08K14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="end : TET3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA020733.1 GI:1484516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA020733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Si
Matches 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA020733/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                           COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

```
// ALCOURT CONTROL CAMPOINT CONTROL CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>;</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H75593 421 bp mRNA EST 01-NOV-1995
yu05f04.rl Soares fetal liver spleen 1NFLS Homo sapiens CDNA clone
                                                                                                                                         Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,M., Le,M.
Mardis,E., Moore,B., Mooris,M., Parsons,J., Prange,C., Rifkin,L.,
Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J.,
Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807\text{-}828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 2350 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       167 CAAGGACTTCTTCAGCATGAAGCCGGAGTGGGAGAACTTGAACCAGTCCAACGTGCGGCG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             595 catgetcaatgateegetgecagaaaaggtgegeatgattaaaeetegaeagtgaaaaggt 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107 CATGCACACTGNCGTGCGGCTGAACGAGGTCATCGTGAAGAAATCCCGGGACGCCAAGCT 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 20; Length 268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="retina"
/dev_stage="55 year old"
/lab_host="DH10B (ampicillin_resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              655 ctactggagcaaacgccatacgcttccctataaaccccatattg 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGTTTTGCTCAACATGCCTGGGCCTCCCCGGAACGGCAATGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="GDB:1280346"
/db_xref="taxon:9606"
/clone="IMAGE:365643"
/clone_lib="Soares retina N2b4HR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Soares and M.Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 3.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.4%; Score 35; 50.6%; Pred. No.
                                                       Mammalia; Eutheria;
1 (bases 1 to 268)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
```

ORGANISM

REFERENCE AUTHORS

ACCESSION VERSION KEYWORDS SOURCE JOURNAL MEDLINE COMMENT

```
AA019639 441 bp mRNA EST 30-JAN-1997 ze62g01.sl Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:363600 3' similar to WP.KO2A2.3 CE02791 BUMETANIDE-SENSITIVE NA-K-C1 COTRANSPORTER;, mRNA sequence.
                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases) 1 to 441.

Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hultman,M., Kucaba,T., Lacy,M., Le,M., M., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Feat: 314 286 1800
Fax: 314 286 1810
Fax: 314 286 1810
Fax: 315 2010 Fax: 1-cdu
This clone is available royalty-free through LLNL; contact the
IMAGE Consorium (Info@image.llnl.gov) for further information.
Insert Length: 2010 Std Error: 0.00
Seq primer: -40M13 fwd. from Amersham
High quality sequence stop: 360.
Localinn/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 167 CAAGGACTICTICAGCATGAAGCCGGAGTGGGAGAACTIGAACCAGTCCAACGTGCGGCG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        catgctcaatgatccgctgccagaaaaggtgcgcatgattaaactcgacagtgaaaaggt 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.4%; Score 35; DB 20; Length 441; larity 50.6%; Pred. No. 4.2; Conservative 0; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="retina"
/dev_stage="55 year old"
/lab_host="DH10B (amplcillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Soares retina N2b4HR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .441
/organism="Homo sapiens"
/db_xref="GDB:1280303"
/db_xref="taxon:9606"
/clone="IMAGE:363600"
                                                                                                                                                                                            AA019639.1 GI:1483067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Wilson RK
                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 83; Conserv
                                                                                                                                                                   AA019639
                                                                                                                                                                                                                                                human.
                                                                     LOCUS
DEFINITION
                           RESULT 5
AA019639/c
                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
JOURNAL
                                                                                                                                                                      ACCESSION
                                                                                                                                                                                            VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Op
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       double stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ő
                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 421)

Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hulman,M., Kucaba,T., Lacy,M., Le,M., E.,Morfe,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schallenberg,K., Soares,M.B., Tan,F., Thierry-Weg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
                                                                                                                                                                                                                                                                                                                                                           Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
97044478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1012 Std Error: 0.00
Seq primer: M13RPl
High quality sequence stop: 366.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1044 actggctggtagaagactttggcttcgaacaatgggatgcctacatgcttctgagtcaat 1103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1104 gcggcaaagtgcggctgggcaacatggtcgaccccaaatacaccgttggcggcgatgctga 1163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242 ACTGGGAAGAGGATGACTTTGGCCTGCGAGGAGATGATCTCAACGCAGGTCTGAGACAAT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                    On Mar 12, 1999 this sequence version replaced gi:4057371.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 86; Length 421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1164 acaaaaacctgttagttagtaggaataactaacc 1198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 35; DB 8
Pred. No. 4.1;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTATACCTTTATAATAGAGCTGATCTTTCTACCC 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
Insert Size: 1012
High quality sequence stops: 366
IMAGE: 232927 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 2.4%;
Best Local Similarity 51.6%;
                      H75593
H75593.1 GI:1049521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .421
                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                        and Marra, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83
```

source

FEATURES

BASE COUNT ORIGIN

Matches

ò q δ 122

δ g

. ;

ö

S

RESULT 6 AA001557/c LOCUS

g à qq DEFINITION

ORGANISM

REFERENCE AUTHORS

ACCESSION VERSION KEYWORDS SOURCE

TITLE JOURNAL COMMENT

```
Unpublished (1997)
Unpublished (1997)
Unpublished (1997)
On Dec 15, 1999 this sequence version replaced gi:4575880.
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: M13 Reverse
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Use of a random BAC End Sequence Database for Sequence-Ready Map
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1122 gcaacatggtcgaccccaaatacaccgttggcgcgatgctgaacaaaaaacctgttagttt 1181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1182 agtaggaataactaaccggtgaacattacccggatgtagatcgggggtaatgtgtaagttc 1241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 691)
Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       595 catgeteaatgateegetgeeagaaaaggtgegeatgattaaaetegacagtgaaaaggt 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B57961 691 bp DNA GSS 20-JUN-1998 CIT-HSP-2011C6.TRB CIT-HSP Homo sapiens genomic clone 2011C6, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="maie" /cell_type="Sperm" /cell_type="Sperm" /note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.4%; Score 35; DB 120; Length 691; Best Local Similarity 52.4%; Pred. No. 4.9; Matches 77; Conservative 0; Mismatches 70; Indels (
                                                                                                                                                                                                                                            655 ctactggagcaaacgccatacgcttccctataaaccccatattg 698
                                                                                                                                                                                                                                                                           225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="GDB:7041464"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="CIT-HSP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        153 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="2011C6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B57961.1 GI:2612295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98
C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "IIIpuiH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                            B57961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                     g
                                                                                                                       ŏ
                                                                                                                                                                             qq
                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                              AA001557 492 bp mRNA EST 29-NOV-1996 ze46d06.sl Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:362027 3' similar to WP:K02A2.3 CE02791 BUMETANIDE-SENSITIVE NA-K-C1 COTRANSPORTER; contains Alu repetitive element;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 3433 Std Error: 0.00
Seq primer: mob.REGA+ET
High quality sequence stop: 233.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
107 CATGCACACTGNCGTGGGCTGAACGAGGTCATCGTGAAGAAATCCCGGGACGCCAAGCT 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 492)
Hillari, Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kucaba, T., Le, M., Lennon, G., Marra, M. Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.4%; Score 35; DB 20; Length 492; 50.6%; Pred. No. 4.4; tive 0; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. 492
/organism="Homo sapiens"
/db_xref="CDB:1278730"
/db_xref="taxon:9606"
/clone="IMAGE:362027"
/clone_lib="Soares retina N2b4HR"
/sex="male"
                                                                                                                       655 ctactggagcaaacgccatacgcttccctataaaccccatattg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Soares and M.Fatima Bonaldo.
141 c 131 g 129 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA001557
AA001557.1 GI:1437022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 83; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                            sednence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80
```

source

FEATURES

ö

0; Gaps

BASE COUNT ORIGIN

29-MAY-1999

ŏ g LOCUS

```
On Dec 15, 1999 this sequence version replaced gi:4215100.
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3867
Fax: (206) 616-3887
Email: jwallacedu washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availablility, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
Plate: 805 row: A column: 17
Seq primer: Sp6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and ECORI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites" 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 422)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D.
    947 tectggecacgaatggagaatgccgaaaatattatgagtattggcagtgcacgteegetg 1006
                                                    238 IGGGTCTACATTAGTGAACCTTTGGATAATTTTATAGGGGTAGAAGGGTCCGGTCCGCTT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       587 ctgacggccatgctcaatgatccgctgccagaaaaggtgcgcatgattaaactcgacagt 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AQ555596 422 bp DNA GSS 29-MAY-1999
HS_5229_A1_A09_SP6E RPCI-11 Human Male BAC Library Homo
sapiens genomic clone Plate=805 Col=17 Row=A, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence-tagged connectors: A sequence approach to mapping scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                 1007 gaggatgcgacgcgaattgcatatcgcgacttaatttactgg 1048
                                                                                                                               DB 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=805 Col=17 Row=A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 34.8; DB:
Pred. No. 4.8;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 422.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                   GI:4915603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.4%;
illarity 49.5%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                   AQ555596.1
                                                                                                                                                                                                                                                                                                                                                sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hood, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOURCE
ORGANISM
                                                                                                                                                                                                                                               AQ555596/c
                                                                                                                                                                                                                                                                                              DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                          KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGIN
                                                 Db
                                                                                                   δ
                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  П
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 396)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pBACe3.6; Site_1: ECORI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of ECORI and ECORI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at ECORI sites"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
0
                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: jwallace 300 or 300 solution.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.mad.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
Plate: 677 row: B column: 2
Seq primer: SP6
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              887 gcagtagagtttgcctcaatcaccaccatcaaagtcgatttgatcaagaactggcagctt 946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        298 ACAGAAGGCCIGGCCAGACAGGICCGAAGGAAIGGIGAGIITICITIGGGGIITAGGGIT 239
                                                                                                                                                                         15-JUN-1999
                                                                                                                                                                                                                 Col=2 Row=B, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               On Feb 19, 1999 this sequence version replaced gi:4146198.
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 105; Length 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db xref="taxon:9606"
/clone="plate=677 Col=2 Row=B"
/sclone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
11 (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
                                                                                                                                                               AQ610392 396 bp DNA GSS 1
HS_5101_B2_A01_SP6E RPCI-11 Human Male BAC Library
Sapiens genomic clone Plate=677 Col=2 Row=B, genomi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tch 2.4%; Score 34.8; DB 105; al Similarity 47.3%; Pred. No. 4.7; 105; Conservative 0; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 396.
Location/Qualifiers
1. .396
1242 aaacaatcgctatttttaacagctaaa 1268
                      543 AATATATCCAAAATATGATCATTTCAA 569
                                                                                                                                                                                                                                                                                                                GI:5071668
                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                             AQ610392.1
                                                                                                                                                                                                                                            sequence.
AQ610392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hood, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local 3
                                                                                                                  RESULT 8
AQ610392/c
                                                                                                                                                                                        DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                    KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
                                                                                                                                                                                                                                                                                                           VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGIN
```

ö

Gaps

; 0

ŏ qq

g ð

^

```
source
                                                                                                                                                                                                                                                                                                         VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                          LOCUS
                                                                                                                                           RESULT 11
AI346857/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                        ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Organ: pooled: Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI. Equal amounts of plasmid DNA from five normalized libraries were maded and so circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneIDs: Soares Nb2HP pool 1: 309384-310919, 32308-328895 Soares Nb2HP pool 1: 145032-147335, 147720-148103, 148872-149255, 15002 - 150407, 151176-15237 Soares Nb2HP pool 1: 758280-760583, 772104-774407 Soares NbHPA pool 1: 730130-720407, 739080-740999 Subtraction by Bento Soares and M. Ratina Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                      AI743670 475 bp mRNA EST 19-DEC-1999
W441e06.x1 Soares_NSF_F8_9W_OT_PA_P_SI Homo sapiens cDNA clone
IMAGE:2367682 3' similar to 9b:223090 HEAT SHOCK 27 KD PROPEIN
(HUMAN);contains MER22.tl TARI repetitive element ; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 475)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NATIONAL Gancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
Email: Robert_Strausbergenih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 823 Std Brror: 0.00
Seg primer: -40UP from Gibco
High quality sequence stop: 437.
Location/Qualiflers
                                                                                           992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   507 aatccatgttgccccgcgggcgttgatccctacggcatctgcgccatgattccgcattttg 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                647 gaaaaggictactggagcaaacgccatacgcitccctataaaccccatattggcaccitg 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                  361 GTATAAGTCTATCAGAGCACATGAGTTTTGATACATTGTAAAGGACACAGTATAATCGAA
                                                                                         707 agcgtatcgccagaaattgactcaatcaattcactgacgccagacaatcacggcgggaat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.4%; Score 34.8; DB 43; Length 475; 60.6%; Pred. No. 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2367682"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AI743670.1 GI:5111958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human.
                                                                                                                                                                                     767 at 768
                                                                                                                                                                                                                                    241 AT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                                                                             AI743670/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
ð
                                            임
                                                                                                                                      q
                                                                                                                                                                                     ò
                                                                                                                                                                                                                                 g
                                                                                           ò
```

```
Homosapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 477)

NOI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NoI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Noitional Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

On Apr 7, 1998 this sequence version replaced gi:3036231.
On Apr 7, 1998 this sequence version replaced gi:3036231.
Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. 477
/organism="Homo saplens"
/organism="Homo saplens"
/db_reref="taxon:9606"
/clone="Ib="NGI_CGAP_CO8"
/tissue_type="adenocarcinoma"
/tissue_type="adenocarcinoma"
/lab host="nDH108"
/note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from colon adenocarcinoma, and was then primed with a Not I - oligo(dT) primer. Dobble-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Patima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                              'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                AI346857 477 bp mRNA EST 30-DEC-1998 qp53e12.xl NCI_CGAP_CO8 Homo sapiens cDNA clone IMAGE:1926766 similar to gb:Z23090 HEAT SHOCK 27 KD PROTEIN (HUMAN);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 38; Length 477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trace considered overall poor quality
Pred. No. 5;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        567 geggaetgaeegggaeeggeeatget 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           257 gcacacreaceregaecececareceaaeer 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 34.8;
Pred. No. 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: -400P from Gibco
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                  AI346857
AI346857.1 GI:4084063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 60.6
Matches 57; Conservative
                                                                                                                                                                                                                                                                                             sednence.
                                                                                                                                                                                                                                                                                                                                                                                                         human.
```

ORGANISM

ACCESSION VERSION KEYWORDS SOURCE

LOCUS

AUTHORS TITLE

JOURNAL

COMMENT

REFERENCE

```
E 1 (bases 1 to 511)
S Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter, J.C.
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
Unpublished (1997)
On Dec 15, 1999 this sequence version replaced gi:4212149.
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: hbe@tigr.org

Clones are derived from the human BAC library RPCI-11. For BAC

Library availability, please context Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from

Research Genet cs (info@resgen.com). BAC end search page:

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.

Seq primer: SP6

Class: BAC ends.
             Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 511)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

[ (Dases 1 to 562)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cell_type="Lymphocytes"
/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIll Human Male BAC Library"
1 79 c 89 g 162 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1198 cggtgaacattacccggatgtagatcggggtaatgtgtaagttcaaacaatcgctatttt 1257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82 CACATICACAGGAACCIGGIGITAGAGCCACAACAIGIGITITIGGAGGGCAIAAIICAA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQ478968 562 bp DNA GSS 23-APR-1999
RPCI-11-269K12.TV RPCI-11 Homo sapiens genomic clone RPCI-11-
269K12, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 103; Length 511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 34.6; DI
Pred. No. 5.9;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1258 taacagctaaagcaggtgcatatggggccagat 1290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCATACTAAGGGCAGTGGCTAGACAGGAAAGAT 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .511
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
/clone="RPCI-11-240H11"
/clone_lib="RPCI-11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="GDB:7591954"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.48; 5
51.68; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AQ478968.1 GI:4661087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
               ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AQ478968/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         202
                                                                                          REFERENCE
                                                                                                                  AUTHORS
                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                    TITLE
                                                                                                                                                                                                                                               COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Mational Carbor in Etitute, Cancer Genome Anatomy Project (CGAP),
Mational Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

N. Unpublished (1997)

On Jun 22, 1998 this sequence version replaced gi:3247021.

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550

Email: Robert Strausbergenh, Gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Prayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 884 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 196.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.45 kb. Life Technologies catalog #:
                                                     AI289776 502 bp mRNA EST 21-DEC-1998 qwl2a01.x1 NCI_CGAP_Ut3 Homo sapiens CDNA clone IMAGE:1990824 3's similar to gb:Z23090 HEAT SHOCK 27 KD PROTEIN (HUMAN);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    507 aatccatgttgccccgcgggcgttgatccctacggcatctgcgccatgattccgcattttg 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    350 AATACACGCTGCCCCGGTGTGGACCCCAACTTTCCTCCTCCTGTCCCATGAGG 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AV482699 511 bp DNA GSS 24-APR-1999
RPCI-11-240H11.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-
AQ482699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. :502
/organism="Homo sapiens"
/db_xref="texon:9606"
/clone="IMAGE:1990824"
/clone=lib="NCI_CGAP_UT3"
/fissue_type="poorly-differentiated endometrial
adenocarcinoma, 2 pooled tumors"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.4%; Score 34.8; DB 37; Length 502; 60.6%; Pred. No. 5.1; Live 0; Mismatches 37; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      567 gcggactgaccggacctgacggccatgct 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 290 GCACACGTGAAGGCCCCCATGCCCAAGCT 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  155 g
                                                                                                                                                            AI289776
AI289776.1 GI:3931617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AQ482699.1 GI:4670103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 57; Conserva
                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                       sednence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91
RESULT 12
A1289776/c
                                                                               DEFINITION
```

FEATURES

BASE COUNT ORIGIN

ò g ŏ g RESULT 13

AQ482699

DEFINITION

ACCESSION VERSION KEYWORDS

SOURCE

ö

Gaps

; 0

```
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                      Email: bbe@tigr.org

Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (lnfo@fresgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 483)
1 (CacAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
Venter, J.C.
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIII Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1198 cggtgaacattacccggatgtagatcggggtaatgtgtaagttcaaacaatcgctatttt 1257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA833827 483 bp mRNA EST 07-APR-1998 od62c06.sl NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1372522 similar to contains MER29.b2 MER29 repetitive element ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         225 CCCCAAACAGAGCCAGGTTATAGAGAACTTTGAATCCCATGTTAAAATACCAACTATTTT 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     285 CACATTCACAGGAACCTGGTGTTAGAGCCACAACATGTGTTTTTGGAGGGCATAATTCAA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On Feb 11, 1998 this sequence version replaced gi:2873159. Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 562;
                                                      Unpublished (1997)
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850
71: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.4%; Score 34.6; DB 103;
51.6%; Pred. No. 6.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1258 taacagctaaagcaggtgcatatggggccagat 1290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCATACTAAGGGCAGTGGCTAGACAGGAAAGAT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .562
/organism="Homo sapiens"
/db_xref="GDB:7603163"
/db_xref="taxon:9606"
/clone="RPCI-11-269K12"
/clone_llb="RPCI-11"
                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA833827.1 GI:2908595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   ends.
                                                                                                                                                                                                                                                                                                                                                                             Seq primer: T7
Class: BAC end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183
                                                                                                                                                                                                                    Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA833827/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                         TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMMENT
                                                                                        COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

```
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bap/image/image.html
Insert Length: 908 Std Brror: 0.00
Seq primer: -40ml3 fwd. ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissuc_type="germinal center B cell"
/lab_host="bHl0B"
/note="vector: pT/T3D-pac (Pharmacia) with a modified
polyliker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, 1gD-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CBER). CDNA synthesis was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ]. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTTT3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ggtgaacattacccggatgtagatcggggtaatgtgtaagttcaaacaatcgctattttt 1258
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     270 GATGATCTTGACCCTGAGTAGGCCTAGGCTAATGTGTAAGGTTTATGTCTTTGTTTTAAC 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                      Ph.D., Gerald Marti, M.D. CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 34.4; DB 31; Length 483; Pred. No. 6.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1259 aacagctaaagcaggtgcatatggggccagatacacccatcaatattg 1306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1372522"
/clone_lib="NCI_CGAP_GCB1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9, 2000, 20:45:53
                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: September
Job time: 2626 sec
                                                                               Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Simi
Matches 62;
                                                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1199
                                                                                                                                                                                                                                                                                              FEATURES
```

***	( MT	****
*******		******
*****	(CCC_CCC)	****
在家家家家家家家家家家家家家家家家家家家家家家家家家家家家家家家家家家家家		***************************************
******		*******
******	<u>'</u>	******
*****	<u> </u>	******
****		*****
****		****

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu Aug 24 18:54:30 2000; MasPar time 10.13 Seconds 767.194 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-214-679-2 (1-328) from US09214679.pep 2417 1 MKWLEESIWAKRGVGAGRKP......GNMVDPKYTVGAMLNKNLLV 328 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

188963 seqs, 23686106 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

a-geneseq36 1:geneseqp Database:

Mean 34.490; Variance 153.853; scale 0.224 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		ď					
Result No.	Score	Query	Length	DB	ID	Description	Pred. No.
	2393	99.0	328	-	W40263	K. oxytoca R-specific	1.62e-213
7	200	8.3	33	Н	W40275		3.33e-07.
3	157	6.5	21	Н	W40272	K. oxytoca R-specific	1.05e-03
4	148	6.1	20	Н	W40264	K. oxytoca R-specific	5.37e-03
ហ	132	5.5	18	~	W40270	K. oxytoca R-specific	9.25e-02
9	132	5.5	575	-	W58856	C. acidivorans gamma-l	9.25e-02
7	122	5.0	19	Н	W40271	K. oxytoca R-specific	5.23e-01
8	122	5.0	23	Н	W40273	K. oxytoca R-specific	5.23e-01
6	107	4.4	482	Н	W08199	B.licheniformis mutant	6.51e+00
10	107	4.4	561	-	W97413	Lucilia cuprina GABA r	6.51e+00
11	104	4.3	14	~	W40274	K. oxytoca R-specific	1.06e+01
12	102	4.2	483	Н	R22750	Alpha amylase.	1.47e+01
13	102	4.2	483	Н	R34289	B. licheniformis alpha	1.47e+01
14	102	4.2	512	-	W10325	B. licheniformis acid	1.47e+01
15	100	4.1	483		W08206	B.licheniformis mutant	2.03e+01
16	100	4.1	483	٦	W05230	Bacillus licheniformis	2.03e+01
17	100	4.1	483	7	R58737	M15E alpha-amylase.	2.03e+01
18	100	4.1	483	7	R58721	M197E alpha-amylase.	2.03e+01
19	100	4.1	483	7	R58003	M366A alpha-amylase.	2.03e+01
20	100	4.1	483		W08193	B.licheniformis mutant	2.03e+01
21	100	4.1	483	Н	W39742	B. licheniformis alpha	2.03e+01
22	100	4 . 1	483	Н	W08211	B.licheniformis mutant	2.03e+01
23	100	4.1	483	П	W31404	Bacillus licheniformis	2.03e+01

	W40263 standard; Protein; 328 AA. W40263; 16-UNN-1998 (first entry) 16-UNN-1998 (first entry) 17-Specific amidohydrolase protein. 18-Specific amidohydrolase; hydrolysis; racemate; nitrogen source; 3,3,3-trifluoro-2-hydroxy-2-methyl propionamide; isoform. 19-UNL-1996; E03670. 10-UNL-1996; CH-001723. 10-JUL-1996; CH-001723. 11-JUNZ ) LONRA AG. 12-JUNZ ) LONRA AG. 13-JUL-1996; CH-001723. 14-JUNZ ) LONRA AG. 15-JUNZ ) LONRA AG. 16-JUNZ ) LONRA AG. 17-JUNZ ) LONRA AG. 18-JUNZ ) LONRA AG. 19-JUL-1996; CH-001723. 10-JUL-1996; CH-001723	tch
R58723 R81476 R58719 R58738 R57999 R57999 R57999 R58727 R58726 R58726 R58726 R58726 R58726 R58726 R58726 R58728 R58007 R71582 Y01582 Y01583 Y01583 Y01583	328 AA.  328 AA.  cohydrolase hydrolysi 2-methyl p  chyl-propio llysis of c mzyme, use German. R-specifi PRS1 which PRS1 which 2-methyl p e is used iluoro-2-hy optical re coptical re cop	SCOTE Pred. 0; h THHLTEEN THHLTEEN NPONGPIN NPONGPIN NPONGPIN NFONGPIN
наннаннаннаннанна	n; III) Rob Rob Groot Gr	08; 48; ve (KPV (IPFL IPFL IPFL 111
4 8 8 3 4 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	rest ent rest ent didition didition didition from A, from A, from A, from A, from A, from A, from A, from B, from B, f	99 conservati AKRCYGAGR. ALLIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHI
	andard;  gg (fi a R-spe a R-spe close of the color a oxyto a oxyto by; cH- gg;	Similari. 26; Con. LEESIMAK. ILEESIMAK. AINSEQDI. AINSEQDI. AINSEQDI. AINSEQDI.
000000000000000000000000000000000000000	1053 st. 0263; 02003; 0300-19;	Ma Ecoc 1 1 21 21
. 4000000000000000000000000000000000000	RESULT AC WA44 AC WA44 AC WAW	Query Best Match 1
	A P P P P P P P P P P P P P P P P P P P	

~

```
W40264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W40270;
                                                                                                                                                           Matches
                                                                                                                                                                                                          32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
            g
                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                            염
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                macroorganism of version of the properties of an R-specific amidohydrolase W40264 W40275 are peptide fragments of an R-specific amidohydrolase isolated from Klebsiella oxytoca strain PRS1. This enzyme allows the microorganism to utilise 3,3,3-trifluoro-2-hydroxy-2-methyl propionamide as its sole nitrogen source. This amidohydrolase is used in a process for a sole nitrogen source. This amidohydrolase is used in a process for the provious of 3,3,3-trifluoro-2-hydroxy-2-methyl propionamide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  preparing (R)-isoforms of 3.3.3-rrifluoro-2-hydroxy-2-methyl propionamide which is cheaper than prior art optical resolution of the racemate using dimethoxy strychnine or (S)-(-)- alpha -methylbenzylamine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
KVDLIKNWQLSWPRMENAENIMSIGSARPLEDATRIAYRDLIYWLVEDFGFEQWDAYMLL 300
                                                                                300
                                                                                                                                                                                                                                                                                                                                                                                              by stereoselective hydrolysis of corresponding racemic amide using microorganism or derived enzyme, used as drug intermediate Example 10.2; Page 29; 68pp; German.
                                                                                                                                                                                                                                                                                                                                                                                  Tri:fluoro-2-hydroxy-2-methyl-propionic acid enantiomer preparation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tri:fluoro.2-hydroxy-2-methyl-propionic acid enantiomer preparation by stereoselective hydrolysis of corresponding racemic amide using microorganism or derived enzyme, used as drug intermediate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                             source;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-JUN-1998 (first entry)
R. oxytoca R-specific amidohydrolase peptide T9-2.
R-specific amidohydrolase; hydrolysis; racemate; nitrogen source; 33,3-trifluoro-2-hydroxy-2-methyl propionamide; isoform.
Klebsiella oxytoca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                         R. oxytoca R. specific amidohydrolase peptide T13-3.
R-specific amidohydrolase; hydrolysis; racemate; nitrogen s 3.3 * trifluoro-2*-hydroxy-2-methyl propionamide; isoform. Klebsiella oxytoca.
W09801568-A2.
15-JAN-1998.
15-JAN-1999; E03670.
03-MAR-1997; CH-000500.
10-JUL-1996; CH-001723.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Indels
                                                                                                                                                                                                                                                                                                                                   Brieden W, Naughton A, Robins K, Shaw N, Tinschert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (LONZ ) LONZA AG.
Brieden W, Naughton A, Robins K, Shaw N, Tinschert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 200; DB 1; I
Pred. No. 3.33e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GVDPYGIEAMIPHFGGLTGTDLTAMLNDQLQPK 33
                                                                                                     328
                                                                                                               301 SQCGKVRLGNWVDPKYTVGAMLNKNLLV 328
                                                                                                 301 SQCGKVRLGNMVDPKYTVGAMLNKNLLV
                                                                                                                                                                            ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard; Protein; 21 AA.
                                                                                                                                                                        standard; Protein; 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.3%;
larity 87.9%;
Conservative
                                                                                                                                                                                                  entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-JUL-1997; E03670.
03-MAR-1997; CH-000500.
10-JUL-1996; CH-001723.
                                                                                                                                                                                                16-JUN-1998 (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                             WPI; 98-101063/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 98-101063/09
                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; V10452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9801568-A2.
                                                                                                                                                                                                                                                                                                                                                   Zimmermann T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JAN-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zimmermann T
                                                                                                                                                           T 2
W40275 S
W40275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "T 3
W40272
                                                241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W40272
 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                             RESULT
 음
                                             d
                                                                                                Dp
                                                                                                                                                                        ò
                                                                       ŏ
                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
```

```
PA (LONZ ) LONZA AG.

PI Brieden W, Naughton A, Robins K, Shaw N, Tinschert A,

Elimeraman T;

Elimeraman T;

Enti-fluoro-2-hydroxy-2-methyl-propionic acid enantiomer preparation

PT Tri:fluoro-2-hydroxy-2-methyl-propionic acid enantiomer preparation

PT Tri:fluoro-2-hydroxy-2-methyl-propionanic acid enantiomer acid enantion and enantiomer preparation acid from Klebsiella cytoca strain PRSI. This enzyme allows the acid solated from Klebsiella cytoca strain PRSI. This enzyme allows the acid isolated from Klebsiella cytoca strain PRSI. This enzyme allows the sistemation acid introgen source. This amidohydrolase is used in a process for preparing (R) isoforms of 3,3,3-trifluoro-2-hydroxy-2-methyl propionamide comparation (R) isoforms of 3,3,3-trifluoro-2-hydroxy-2-methyl propionamide comparation art optical resolution of the racemate using committee.
Example 10.2; Page 29; 68pp; German.

Wav0264-WAV0275 are peptide fragments of an R-specific amidohydrolase isolated from Riebsialla oxytoca strain PRS1. This enzyme allows the microorganism to utilise 3,3 atrifluoro-2-hydroxy-2-methyl propionamide as its sole nitrogen source. This amidohydrolase is used in a process for preparing (R)-isoforms of 3,3,3-trifluoro-2-hydroxy-2-methyl propionamide which is cheaper than prior art optical resolution of the racemate using dimethoxy strychnine or (S)-(-)- alpha -methylbenzylamine.
                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-JUN-1998 (first entry)

K. Oxytoca R-specific amidohydrolase peptide T8.

R. Specific amidohydrolase; hydrolysis; racemate; nitrogen source; 3, 3, 3-trifluoro-2-hydroxy-2-methyl propionamide; isoform.

Klebsiella oxytoca.
                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nitrogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-JUN-1998 (first entry)
K. oxytoca R-specific amidohydrolase N-terminal peptide.
R-specific amidohydrolase; hydrolysis; racemate; nitrogen 3,3,3-trifluoro-2-hydroxy-2-methyl propionamide; isoform.
                                                                                                                                                                                                                                                                Score 157; DB 1; Length 21; Pred. No. 1.05e-03;
                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brieden W, Naughton A, Robins K, Shaw N, Tinschert A,
                                                                                                                                                                                                                                                                                           Pred. No. 1.05e-0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.1%; Score 148; 95.0%; Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard; Protein; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W40270 standard; Protein; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                          21
                                                                                                                                                                                                                                                                                                                                                                                                                         52
                                                                                                                                                                                                                                                             Query Match 6.5%;
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20
                                                                                                                                                                                                                                                                                                                                                                                                   EFHYTIGPYSTPVLTIEPGDR
                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKWLEESIMAKRGVGAGRKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKWLEESIMAKRGVGASRKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-JUL-1997; E03670.
03-MAR-1997; CH-000500.
10-JUL-1996; CH-001723.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JAN-1998.
10-JUL-1997; E03670.
03-MAR-1997; CH-000500.
10-JUL-1996; CH-001723.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Klebsiella oxytoca.
W09801568-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (LONZ ) LONZA AG.
                                                                                                                                                                                                                                                                                                                 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JAN-1998
                                                                                                                                                                                                               Sequence
```

¥

```
WPI; 98-1010

WPI; 98-101063/09.

Tri:fluoro-2-hydroxy-2-methyl-propionic acid enantiomer preparation

-by stereoselectrive hydrolysis of corresponding racemic amide using

microorganism or derived enzyme, used as drug intermediate

Example 10.2; Page 29; 68pp; German.

W40264-W40275 are peptide fragments of an R-specific amidohydrolase

isolated from Klebsiella oxytoca strain PRS1. This enzyme allows the

microorganism to utilise 3,3,3 trifluoro-2-hydroxy-2-methyl propionamide

as its sole nitrogen source. This amidohydrolase is used in a process for

preparing (R)-isoforms of 3,3,3-trifluoro-2-hydroxy-2-methyl propionamide

which is cheaper than prior art optical resolution of the racemate using

dimethoxy strychnine or (S)-(-)- alpha -methylbenzylamine.
                                                                     16-JUN-1998 (first entry)

K. oxytoca R-specific amidohydrolase peptide T9-1.

R-specific amidohydrolase; hydrolysis; racemate; nitrogen source; 3, 3, 3-trifluoro-2-hydroxy-2-methyl propionamide; isoform.
                                                                                                                                                                                                                                                                                                                                        (LONZ ) LONZA AG.
Brieden W, Naughton A, Robins K, Shaw N, Tinschert A,
T
W40271 standard; Protein; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DAFEGAINSEQDIPSQLLK 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 DAFEGAINSEQDIPSQLLK 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 5.0%;
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19; Conservative
                                                                                                                                                                                                                               15-JAN-1998.
10-JUL-1997; E03670.
03-MAR-1997; CH-000500.
10-JUL-1996; CH-001723.
                                                                                                                                                                                   Klebsiella oxytoca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (LONZ ) LONZA AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9801568-A2.
                                                                                                                                                                                                               WO9801568-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zimmermann
                                                                                                                                                                                                                                                                                                                                                                                                  Zimmermann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W40273;
                                              W40271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                             Example 10.2; Page 29; 68pp; German.

W40264-W40275 are peptide fragments of an R-specific amidohydrolase isolated from Klebsiella oxytoca strain PRS1. This enzyme allows the microorganism to utilise 3.3,3-trifluoro-2-hydroxy-2-methyl propionamide as its sole nitrogen source. This amidohydrolase is used in a process for preparing (R)-isoforms of 3,3,3-trifluoro-2-hydroxy-2-methyl propionamide which is cheaper than prior art optical resolution of the racemate using dimethoxy strychnine or (S)-(-)- alpha -methylbenzylamine.
                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This engryer of the bicyclic lactamase capable of hydrolysing an enantiomer of the bicyclic lactam 2-azabicyclo(2.2.1)hept-5-en-3-one. This engryme has at least 1 of the following features; greater than 85% retention of activity after incubating at 40 deg. C for 4 hours, or 30% activity after incubating at 60 deg. C for 4 hours, or an initial concentration of 100 g racemic lactam plus 300 ml buffer and proceeding to at least 90 (especially at least 98)% hydrolysis of the (+) lactam with <5% hydrolysis of the (-) lactam. The enzyme is much more temperature-stable than previously identified (+)-gamma-lactamases carried out at very high substrate/product concentrations. This enzyme has applications as a therapeutic agent e.g. as an antiviral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ĥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240 EGARTVPPREHGGNCDIKDLSRGSRVFFPVYVDGAGLSVGDLHFSQGDGEITFWGPIEMP 299
             Tri:fluoro-2-hydroxy-2-methyl-propionic acid enantiomer preparation by stereoselective hydrolysis of corresponding racemic amide using microorganism or derived enzyme, used as drug intermediate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lactamase enzyme specifically hydrolysing (+)-enantiomer of 2-aza:bi:cyclo(2.2.1)hept-5-en-3-one - isolated from Comamonas acidivorans or prepared by recombinant DNA technology, used as, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C. acidivorans gamma-lactamase protein. Gamma-lactamase, enantiomer; bicyclic lactam; temperature stable; 2-azabicyclo(2.2.1)hept-5-en-3-one; therapeutic agent; antiviral; cardac vasodilator.
                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 132; DB 1; Lengum J. Pred. No. 9.25e-02;
                                                                                                                                                                                                                                                                                                                                                                       Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                    Score 132; DB 1; 1
Pred. No. 9.25e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 5; Page 17-20; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W58856 standard; Protein; 575 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                        :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RC, Lee CS, Wisdom RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 5.5%;
Best Local Similarity 38.0%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                    Query Match 5.5%;
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78 MPFLNPQNGPIMVNGAEK 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MPFLNPQNGPIMVNGAEK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                        18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-MAR-1998.
01-SEP-1997; G02344.
03-SEP-1996; GB-018340.
(CHIR-) CHIROSCIENCE LT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Comamonas acidivorans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 98-193625/17.
N-PSDB; V11459.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cardiac vasodilator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 575 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9810075-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W58856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brown
                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
```

a

ŏ

ö

Gaps

ö

Length 19; 0; Indels

Score 122; DB 1; I Pred. No. 5.23e-01; 0; Mismatches

```
Zimmermann 1:

WPI; 98-101063/09.

Tri:fluoro-2-hydroxy-2-methyl-propionic acid enantiomer preparation

- by stereoselective hydrolysis of corresponding racemic amide using microorganism or derived enzyme, used as drug intermediate microorganism or derived enzyme, used as drug intermediate

Example 10.2; Page 29; 68pp; German.

W40264-W40275 are peptide fragments of an R-specific amidohydrolase isolated from Klebsiella oxytoca strain PRSI. This enzyme allows the microorganism to utilise 3,3 -trifluoro-2-hydroxy-2-methyl propionamide as its sole nitrogen source. This amidohydrolase is used in a process for preparing (R)-isoforms of 3,3 -trifluoro-2-hydroxy-2-methyl propionamide which is cheaper than prior art optical resolution of the racemate using dimethoxy strychnine or (S)-(-)- alpha -methylbenzylamine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                           K. oxytoca R-specific amidohydrolase peptide T11.
R-specific amidohydrolase, hydrolysis; racemate; nitrogen source; 3,3,3-trifluoro-2-hydroxy-2-methyl propionamide; isoform.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 122; DB 1; Length 23;
Pred. No. 5.23e-01;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                           Brieden W, Naughton A, Robins K, Shaw N, Tinschert A,
                       Ā
JT 8
W40273 standard; Protein; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 91.3%;
21; Conservative
                                                          16-JUN-1998 (first entry)
                                                                                                                                                                                                           10-JUL-1997; E03670.
03-MAR-1997; CH-000500.
10-JUL-1996; CH-001723.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 21; Conser
                                                                                                                                                Klebsiella oxytoca
```

: :|| ||| 236 SITTIKVDLIK 246 300 GWVHMKVSLIK 310

g

ò

셤 δ US-09-214-679-2.rag

```
g
88888
                                                                                                         a
                                                                                                                                 ò
                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                οχ
                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel mutant alpha-amylases contain a deletion or substitution of at least one asparagine residue from the wild-type. The present sequence is a specific example of such a mutant alpha-amylase from which the His residue at position 13 has been deleted. The mutant alpha-amylase is useful for starch processing and liquefaction. It is used in dishwashing or fabric-cleaning detergent compositions. The modifications produce enzymes with enhanced low pH performance suited for commercial liquefaction conditions. The mutant alpha-amylases are also found to have improved thermal and oxidative stability and to be more stable in the absence of calcium ions, compared to wild-type.

N.B. The present sequence is not shown in the specification but is derived from the Bacillus licheniformis alpha-amylase sequence shown in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QKGTVRTKYGTKGELQSA-IKSLHSRDINVYGD-VVINHKGGADATEDVTAVEVDP-ADR 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mutant alpha-amylase with improved low pH starch hydrolysis activity - has at least one asparagine residue substituted or deleted, useful in detergents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     \ensuremath{\mathsf{GABA}} receptor sub-unit from L. cuprina - used in the production of effective pesticides
                                                                                                                               Asparagine; substitution; mutation; dish-washing; fabric-cleaning;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gamma-aminobutyric acid receptor; GABA receptor; sheep blow fly;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 107; DB 1; Length 482
Pred. No. 6.51e+00;
21; Mismatches 27; Indels
                                                                                                     16-JUL-1997 (first entry)
B.licheniformis mutant alpha-amylase, His 133 deletion.
                                                                                                                                                                                                                                         Ropp T;
                                                                                                                                                                                                                                        Requadt C, Ringer C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lucilia cuprina GABA receptor subunit.
                      JT 9
WO8199 standard; protein; 482 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W97413 standard; Protein; 561 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 1; 2pp; English.
                                                                                                                                                                                                                                                                                                            Page -; 49pp; English
         1 LFIGDAHAEQGDGEIEGTAVEFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 4.4%;
Local Similarity 31.2%;
Les 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143 VRMIKLDSEKVYWSKRH 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 NRVISGELIKA-WTHFH 141
                                                                                                                                                                                       12-DEC-1996, 009089. 06-JUN-1995; US-468700. (GEMV ) GENENCOR INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-OCT-1997; 403074.
20-OCT-1997; RD-403074.
                                                                                                                                                    Bacillus licheniformis
                                                                                                                                                                                                                                        Mitchinson C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ANON ) ANONYMOUS.
WPI; 98-007412/01.
N-PSDB; X16065.
                                                                                                                                                                                                                                                  Solheim LP;
WPI; 97-043150/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             482 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lucilia cuprina.
RD-403074-A.
                                                                                                                                                                             WO9639528-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-NOV-1997.
                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pesticide.
                                                                                                                                            detergent
                                                                                                                                                                                                                                                                                                            Claim 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     figure 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W97413;
                                                                                             W08199
                                                                                                                                                                                                                                         Day A,
                                 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
                                                                                ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δλ
```

```
Tri:fluoro-2-hydroxy-2-methyl-propionic acid enantiomer preparation
- by stereoselective hydrolysis of corresponding racemic amide using
- by stereoselective hydrolysis of corresponding racemic amide using
- by stereoselective hydrolysis of corresponding racemic amide using
- by stereoselective hydrolysis of corresponding racemic amide using
- by stereoselective hydrolysis of corresponding intermediate
- by 68pp; German.
- M40264 W40275 are peptide fragments of an R-specific amidohydrolase
- isolated from Klebsiella oxytoca strain PRSI. This enzyme allows the
- microorganism to utilise 3,3,3-trifluoro-2-hydroxy-2-methyl propionamide
- as its sole nitrogen source. This amidohydrolase is used in a process for
- preparing (R)-isoforms of 3,3,3-trifluoro-2-hydroxy-2-methyl propionamide
- which is cheaper than prior art optical resolution of the racemate using
- dimethoxy strychnine or (S)-(-)- alpha - methylbenzylamine.
                                                                                                                                                                                                 Gaps 15;
                                                                                                                                                                                                                                                                                   28 LAM-FLQEPKKQITIVNAATAGGSMLGDVNVSAILDSFSVSYDK-RVRPNYGGPPVEVGV 85
The present sequence represents a gamma-aminobutyric acid (GABA) receptor subunit from the sheep blow fly, Lucilia cuprina. The GABA receptor subunit protein may be used to develop novel pesticides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lo-JUN-1998 (first entry)

K. oxytoca R-specific amidohydrolase peptide T13-1.

R-specific amidohydrolase; hydrolysis; racemate; nitrogen source; 3,3,3-trifluoro-2-hydroxy-2-methyl propionamide; isoform.

Klebsicila oxytoca.

WO980158-A2.

I5-JAN-100-
                                                                                                                                                                                                                                                                                                                                                                                                 86 TMYVLSISSLSE-VKMDFTLDFYFRQFWTDPR-LAYGKRPGVETLSVGSEFIKNI 138
                                                                                                                                     Score 107; DB 1; Length 561;
Pred. No. 6.51e+00;
28; Mismatches 36; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Heat stable; mutant; textile processing; papermaking; brewing;
starch; hydrolysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 104; DB 1; Length 14; Pred. No. 1.06e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Phe, Leu, Tyr, Glu, Lys, or Gln"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (LONZ ) LONZA AG.
Brieden W, Naughton A, Robins K, Shaw N, Tinschert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R22750 standard; Protein; 483 AA.
                                                                                                                                          4.4%;
ilarity 31.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hest Local Similarity 100.08;
Matches 14; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FR-009679.
NAT RECH AGRON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JAN-1998.
10-JUL-1997; E03670.
03-MAR-1997; CH-000500.
10-JUL-1996; CH-001723.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus licheniformis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14
                                                                                                                                     Query Match
Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GDVLAVYIESMLPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  009679
                                                                                   561 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alpha amylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-JAN-1992.
30-JUL-1990; 0
30-JUL-1990; F
(INRG ) INST N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zimmermann T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FR2665178-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R22750;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96
```

ö

Ŋ Page

Gaps

4

Indels

```
69 QKGTVRTKYGTKGELQSA-IKSLHSRDINVYGD-VVINHKGGADATEDVTAVEVDP-ADR 125
                                                                                 |:| : : : ||: : : | |: :: | 84 QNGPIMVNGAEKGDVLAVYIESMLPRGYDPYGICAMIPHFGGLTGT-DLTAMLNDPLPEK 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98 QKGTVRTKYGTKGELQSA-IKSLHSRDINVYGD-VVINHKGGADATEDVTAVEVDP-ADR 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-JUL-1997 (first entry)
B.licheniformis mutant alpha-amylase, M15T/N188S/A209V substitution.
Asparagine; substitution; mutation; dish-washing; fabric-cleaning;
                                                                                                                                                                                                                                                                                                                                                        B. licheniformis acid stable and thermostable alpha-amylase. Acid stable; thermostable; alpha-amylase; mutation; mutant; 134Arg; 310Gly; 320Ala; recombinant production; investigation; enzyme. Bacillus licheniformis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene encoding acid-stable and thermostable alpha-amylase -
comprising Bacillus licheniformis enzyme having arginine, glycine
and alanine at positions 134, 310 and 320, respectively
Claim 1; Pages 7-8; 9pp; Japanese.
The present sequence is an acid stable and thermostable Bacillus
licheniformis alpha-amylase (AA), comprising the mutations 134Arg,
310Gly and 320Ala. The AA gene can be used for the recombinant
prodn. Of the mutant AA, which may be useful for investigating the
effects of specific amino acid substitutions on the enzyme's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "wild type residue substd. with Arg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "wild type residue substd. with Gly"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "wild type residue substd. with Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 102; DB 1; Length 512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 1.47e+01;
21; Mismatches 29; Indels
       21; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . .29
label=_sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30. .512
/label= mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JT 15
W08206 standard; protein; 483 AA.
                                                                                                                                                                                                                                                                                           W10325 standard; Protein; 512 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity 29.9%;
Matches 23; Conservative
       Conservative
                                                                                                                                              126 NRVISGEXLIKAWTHFH 142
                                                                                                                                                                                             143 VRMIKLDSEKVYWSKRH 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       155 NRVISGEHRIKAWTHFH 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   143 VRMIKLDSEKVYWSKRH 159
                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-NOV-1996.
20-APR-1995; 119386.
20-APR-1995; JP-119386.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SANS-) SANSHO KAKO KK. WPI; 97-028344/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       detergent.
Bacillus licheniformis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               512 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_difference 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; T47072.
       23;
                                                                                                                                                                                                                                                                                                                                       14-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J08289788-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W08206;
                                                                                                                                                                                                                                                                                                                   W10325;
       Matches
                                                                                                                                              qq
                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                              4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A series of alpha-amylase mutants was prepared by site-directed mutagenesis at amino acid position 133. Substitution of wild-type (so this by pro, Ser, Gly or Ala (all are less hydrophobic than His) resulted in proteins with less residual activity after heating than the native enzyme. Replacement of His by Glu, Lys, Glu, Lu, phe or Tyri (increasingly more hydrophobic than His) resulted in proteins with a greater residual activity after heating than proteins with a greater residual activity after heating than his. The Tyri33 mutant had a half-life at 90 deg.C of 8 mins, c.f. of mins for the wild-type enzyme. Substitution of Ala209 by a more hydrophobic amino acid also enhances the enzyme's thermostability. When the enzyme carries mutations at both positions 133 and 209 it has a half-life at 90 deg.C that is 9-10 times greater than the native enzyme. The mutant alpha-amylases are useful in the brewing, see also Ril362.3, R34288 and R34290.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        OKGTVRTKYGTKGELQSA-IKSLHSRDINVYGD-VVINHKGGADATEDVTAVEVDP-ADR 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |:| : : | |:: : | |:: | | :: | | 34 QNGPIMVNGAEKGDVLAVYIESMLPRGVDPYGICAMIPHFGGLTGT-DLTAMLNDPLPEK 142
                                                               Heat stable variant of Bacillus licheniformis alpha amylase with specific substitution around position 113, useful in paper mfg., brewing, etc. for starch liquefaction [Claim 2, Fig 1; 17pp; French.

The alpha-amylase protein sequence shown differs from the wild-type enzyme by having His 133 mutated to an amino acid that is more hydrophobic than His (see features). The heat stable alpha amylases are useful in textile processing, papermaking and brewing, specifically for hydrolysis (liquifaction) of starch.
                                                                                                                                                                                                                                                                                                                                                                                                              4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B.licheniformis alpha amylase mutein with substn. at position 133. thermostability; site-directed mutagenesis.

Bacillus licheniformis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               have specific aminoacid substitutions at positions 133 and/or 209 for simultaneous gelation and liquefaction of starch e.g. in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Phe, Gln, Glu, Lys, Leu, Tyr
/note= "substn. of wild-type Hisl33 by a more
hydrophobic amino acid, esp. Tyr,
amylase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New heat stable forms of Bacillus licheniformis alpha-amylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 102; DB 1; Length 483;
Pred. No. 1.47e+01;
                                                                                                                                                                                                                                                                                                                                                               Length 483;
                                                                                                                                                                                                                                                                                                                                                                                                            21; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                             Score 102; DB 1; 1
Pred. No. 1.47e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (INRG ) INRA INST NAT RECH AGRONOMIQUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Declerck K, Gaillardin C, Joyet P; WPI; 93-020251/03.
Declerck N, Joyet P, Gaillardin C; WPI; 92-116558/15.
N-PSDB; Q23551.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /T 13
R34289 standard; Protein; 483 AA.
R34289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Fig 1; 23pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 4.2%;
Best Local Similarity 29.9%;
                                                                                                                                                                                                                                                                                                                                                           / Match 4.2%;
Local Similarity 29.9%;
les 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 NRVISGEXLIKAWTHFH 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143 VRMIKLDSEKVYWSKRH 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-MAY-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-MAY-1991; FR-005740.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-NOV-1992,
13-MAY-1991; 005740.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_difference 133
                                                                                                                                                                                                                                                                                                            483 AA;
                                                                                                                                                                                                                                                                                 See also R25434
                                                                                                                                                                                                                                                                                                                                                                                                         23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FR2676456-A
                                                                                                                                                                                                                                                                                                                 Seguence
                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
```

69 Matches

g ô рp ò

RESULT

4; Gaps

brewing

DAC NAME OF THE PROPERTY OF TH

```
misc_difference 188

Tote= "Wild-type Met substituted by Thr"

The misc_difference 188

FT misc_difference 188

FT misc_difference 209

FT Moofs 39528-A2.

PM W09639528-A2.

PM W09639528-A2.

PM W09639528-A2.

PM W09639528-A2.

PM W12-1995; UG-468700.

GEMV. 1995; UG-468700.

GEMV. 1997-043150/04.

PM WICH 1997-043150/04.

PM WHOTH 1997-043150/04.

PM WHOTH 1997-043150/04.

PM WOFF 1997-043150/04.

PM WOFF 297-043150/04.

PM WOFF 297-043150/04.

PM WAT: 97-043150/04.

PM WAT: 97-043150/04.

PM WAT: 97-043150/04.

PM WOFF 297-043150/04.

PM WOFF 297-043150/04.

PM WAT: 97-043150/04.

PM WAT: 97-043150/04.

PM WAT: 97-043150/04.

PM WAT: 97-043150/04.

CC Laim 7; Page -: 49pp; English

CC Taim 7; Page -: 49pp; English

CC Taim 7; Page -: 49pp; English

CC The Matent alpha-amylases contain a deletion or substituted by a Val residue.

CC The Matent alpha-amylase is useful for starch processing and the An residue at position 209 has been substituted by a Val residue.

CC The mutant alpha-amylase is useful for starch processing and the Moofilications produce enzymes with enhanced low ph CC CMPOSITIONS. The modifications produce enzymes with enhanced low ph CC CMPOSITIC ADPA - amylases are also found to have improved thermal and oxidative conspositions. The present sequence is not shown in the specification but is Sequence to MB Tigure 4.

CC Garived from the Bacillus licheniformis alpha-amylase sequence shown in Sequence 483 AA;
```

69 QKGTVRTKYGTKGELQSA-IKSLHSRDINVYGD-VVINHKGGADATEDVTAVEVDP-ADR 125

Query Match
4.1%; Score 100; DB 1; Length 483;
Best Local Similarity 29.9%; Pred. No. 2.03e+01;
Matches 23; Conservative 21; Mismatches 29; Indels 4; Gaps

*	(TM)
***************************************	
	[
t t t t	
t t t t	
t t t t t	

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

Thu Aug 24 18:55:16 2000; MasPar time 7.21 Seconds 697.344 Million cell updates/sec Run on:

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated.

>US-09-214-679-2 (1-328) from USO9214679.pep 2417 1 MKWLEBSIMAKRGVGAGRKP......GNMVDPKXTVGAMLNKNLLV 328 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

152433 seqs, 15329240 residues Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries

a-issued 1:5A\_COMB 2:5B\_COMB 3:6\_COMB 4:PCT\_COMB 5:backfiles1 Database:

Mean 32.340; Variance 149.359; scale 0.217 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ			CHANGE			
Result No.	Score	Query	Length	DB	G.	Description	ά	Pred. No.
1	102	4.2	483	7	US-08-645-	Sequence 2, Applicatio	1	8.46e+00
7	100	4.1	483	7	US-08-468-	36,	ti.	1,17e+01
E	100	4.1	483	7	US-08-468-	32,	ti.	1.17e+01
4	100	4.1	483	٦	US-08-468-	34,	ti.	1.17e+01
S	100	4.1	483	٣	US-08-914-	3, A	10	1.17e+01
9	100	4.1	483	7	US-08-704-	34,	t.	1.17e+01
7	100	4.1	483	7	US-08-468-	36,	ti.	1.17e+01
80	100	4.1	483	m	-068-80-sn	3, A	io	1.17e+01
თ	100	4.1	483	4	PCT-US95-1	Sequence 32, Applicati	ţ.	1.17e+01
10	100	4.1	483	4	PCT-US94-0	36,	ti.	1.17e+01
11	100	4.1	483	4	PCT-US94-0	Sequence 32, Applicati	ti.	1.17e+01
12	100	4.1	483	4	PCT-US95-1	Sequence 36, Applicati	ti.	1.17e+01
13	100	4.1	483	~	US-08-468-	Sequence 32, Applicati	ţï	1.17e+01
14	100	4.1	487	~	us-08-468-	37,	ti.	1.17e+01
15	100	4.1	487	4	PCT-US94-0	Sequence 37, Applicati	ti.	1.17e+01
16	100	4.1	487	7	US-08-468-	Sequence 37, Applicati	ti.	1.17e+01
17	100	4.1	487	4	PCT-US95-1	Sequence 37, Applicati	ti.	1.17e+01
18	100	4.1	511	4	PCT-US95-1	Sequence 33, Applicati	ti	1.17e+01
19	100	4.1	511	m	US-08-914-	Sequence 2, Applicatio	io	1.17e+01
20	100	4.1	511	m	US-08-914-	Sequence 4, Applicatio	10	1.17e+01
21	100	4.1	511	m	-068-80-SN	Sequence 4, Applicatio	io	1.17e+01
22	100	4.1	511	Н	US-08-468-	Sequence 35, Applicati	ti.	1.17e+01
23	100	4.1	511	Н	US-08-645-	Sequence 3, Applicatio	io	1.17e+01

1.17e+01 1.1				•	•	pə				Gaps 4;	-ADR 125 ::: DEK 142	:	
Applicati Applicati Applicati Applicatio						ving Alter	25 (EPO)			gth 483; Indels 4;	EDVTAVEVDP-AD  :  :   :: -DITAMINDPLDE		
Sequence 33, Sequence 33, Sequence 33, Sequence 2, Sequence 2, Sequence 2, Sequence 2, Sequence 2, Sequence 2, Sequence 5, Sequence 6, Sequence 6, Sequence 6, Sequence 6, Sequence 6, Sequence 8, Sequence 8, Sequence 2, Sequence 2, Sequence 2, Sequence 3, Sequence 3, Sequence 2, Sequence 2, Sequence 2, Sequence 2, Sequence 2, Sequence 2, Sequence 3, Sequence 4, Sequence 5, Sequence 6, Seq		483 AA.				•—	Version #1.	71	ν. 	DB 1; Len .46e+00; ches 29;	QKGTVRTKYGTKGELQSA-IKSLHSRDINVYGD-VVINHKGGADATEDVTAVEVDP  :	† † †	
PCT-US94-0 US-08-704- US-08-468- US-08-468- US-08-468- US-08-683- US-08-683- US-08-600- US-08-600- US-08-812- US-08-812- US-08-814- US-08-	ALIGNMENTS	D; PRT;		08645971	/08645971	Modified Alpha-Amylases Calcium Binding Propert 5 M:	Floppy disk  M PC compatible  STEM: PC-DOS/MS-DOS  atentIn Release #1.0.	08/645,9	icheniformis	Score 102; DB Pred. No. 8.46e 21; Mismatches	LHSRDINVYGD ::   ::     Mr.prcvnpyg1		
5111 2 5111 2 5111 2 5111 2 5111 2 5111 2 512 2 512 2 512 2 512 2 512 2 512 2 512 2 512 2 512 2 512 2 512 2 512 3		STANDARD		Application US/0864597	ion :	TITLE OF INVENTION: MG TITLE OF INVENTION: Ca NUMBER OF SEQUENCES: 5 COMPUTER READABLE FORM:	E: Floppy IBM PC COM SYSTEM: PC Patentin R	CURRENT APPLICATION DATA: APPLICATION NUMBER: US/ INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 483 amino acids	TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear LECULE TYPE: protein IGINAL SOURCE: ORGANISM: Bacillus 1: ORGANISM: As: 55268 WM	4.2%; Similarity 29.9%; 23; Conservative	KGELQSA-IKS   ::::	AWTHFH 142	15
44444444444444444444444444444444444444		5-971-2		2,	Sequence 2, Applicat. Patent No. 5763385 GENERAL INFORMATION APPLICANT:	TITLE OF INV TITLE OF INV NUMBER OF SE COMPUTER REA	MEDIUM TYPE COMPUTER: OPERATING SY SOFTWARE:	ENT APPL PLICATIO ATION FO ENCE CHA	TYPE: amino a STRANDEDNESS: TOPOLOGY: lin MOLECULE TYPE: ORIGINAL SOURCE: ORGANISM: BACCE 483 AA; AB ABCE 483 AA;	Similari 23; Con	TVRTKYGT : : :	NRVISGEHRIKAWTHFH	:  :  :   VRMIKLDSEKVYWSKRH
1000 1000		r 1 US-08-64	xxxxx	Sequence	Seg Sat GE		S O O	CURE AP INFORM SEQU	TYPE: STRAND TOPOLO MOLECULE ORIGINAL ORGANI	/ Match Local nes	69 QKG   -     84 ONG	و ،	С
200222888888884444444444444444444444444		RESUI ID	X X X X	X E	×ଧଧଧଧ	8888	8888	888888		Que Bes Mat	g &	연	Qy

```
Sequence 32, Application US/08468698
Patent No. 5845549
GENERAL INFORMATION:
APPLICANT: Antrim, Richard L.
APPLICANT: Barnett, Christopher APPLICANT: Mitchinson, Colin
APPLICANT: Power, Scott D.
APPLICANT: Requadt, Carol
APPLICANT: Leif P.
TITLE OF INVENTION: Oxidatively Stable Alpha-Amylase
                                                                                                                                                                                                                                                                                                                                                                        COMPUTE READDLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb
COMPUTER: TBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,698
FILING DATE: 06-JUN-95
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                        ADDRESSEE: Genencor International, Inc.
STREET: 180 Kimball Way
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LE TYPE: protein
483 AA; 55211 MW; 1221290 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/194,664
FILING DATE: 10-FEB-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/016,395
FILING DATE: 11-FEB-93
ATTORNEY/AGENT INFORMATION:
                                                                             Sequence 32, Application US/08468698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Stone, Christopher L. REGISTRATION NUMBER: 35,696 REFERENCE/DOCKET NUMBER: GTELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (415) 742-7217
INFORMATION FOR SEQ ID NO: 32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (415) 742-7555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 483 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: 111
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                               94080
                                                                                                                                                                                                                                                                                                                                        CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LT 4
US-08-468-700-34
                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                       xxxxxx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 QKGTVRTKYGTKGELQSA-IKSLHSRDINVYGD-VVINHKGGADATEDVTAVEVDP-ADR 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4;
                                                                                                                                                                           APPLICANT: Antrim, Richard L.
APPLICANT: Barnett, Christopher
APPLICANT: Mitchinson, Colin
APPLICANT: Power, Scott D.
APPLICANT: Requadt, Carol
APPLICANT: Requadt, Carol
APPLICANT: Solheim, Leif P.
NUMBER OF SEQUENCES: 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 4.1%; Score 100; DB 2; Length 483; Best Local Similarity 29.9%; Pred. No. 1.17e+01; Matches 23; Conservative 21; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                  483 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    483 AA.
                                                                                                                                                                                                                                                                                            AUNKESSEE: Genencor International, Inc. STREET: 180 Kimball Way
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/468,220
FILING DATE: 06-JUN-95
CLASSIETCATION: 435
PRIOR APPLICATION DATE:
APPLICATION NUMBER: 08/194,664
FILING DATE: 10-FEB-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/016,395
FILING DATE: 11-FEB-93
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 483 AA; 55181 MW; 1222078 CN;
                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GC220D1
                                                                                                                                 Sequence 36, Application US/08468220 Patent No. 5824532 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Stone, Christopher L.
REGISTATION NUMBER: 35,696
REFERENCE/DOCKET NUMBER: GC220
TELECOMMUNICATION INFORMATION:
TELEFONE: (415) 742-7555
TELEFAX: (415) 742-7217
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                                                    Sequence 36, Application US/08468220
                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 483 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126 NRVISGEHLIKAWTHFH 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143 VRMIKLDSEKVYWSKRH 159
               US-08-468-220-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-468-698-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                              XXXXXX
RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
ID US
                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

GC220D2

```
69 QKGTVRTKYGTKGELQSA-IKSLHSRDINVYGD-VVINHKGGADATEDVTAVEVDP-ADR 125
                                                       4; Gaps
Query Match 4.1%; Score 100; DB 2; Length 483; Best Local Similarity 29.9%; Pred. No. 1.17e+01; Matches 23; Conservative 21; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                             483 AA.
                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                           126 NRVISGEHLIKAWTHFH 142
                                                                                                                                                                                                                                           143 VRMIKLDSEKVYWSKRH 159
```

m

```
TITLE OF INVENTION: MUTANT ALPHA-AMYLASE COMPRISING MODIFICATION
TITLE OF INVENTION: AT RESIDUES CORRESPONDING TO A210, H405 AND/OR
TITLE OF INVENTION: T412 IN BACILLUS LICHENIFORMIS
CORRESPONDENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: Genencor International, Inc.
STREET: 925 page Mill Road
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 QKGTVRTKYGTKGELQSA-IKSLHSRDINVYGD-VVINHKGGADATEDVTAVEVDP-ADR 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
4.1%; Score 100; DB 3; Length 483;
Best Local Similarity 29.9%; Pred. No. 1.17e+01;
Matches 23; Conservative 21; Mismatches 29; Indels
                                                                                                                                                                                 COUNTRY: USA
ZIP: 94304-1013
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION DATE: US/08/914,679A
FILING DATE: TO BE ASSIGNED
ATTORNEY ACENT INFORMATION:
NAME: Stone, Christopher
REGISTRATION NUMBER: 35,696
REFERENCE/DOCKET NUMBER: 35,696
REFERENCE/DOCKET NUMBER: 35,696
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 846-7555
TELEPHONE: (650) 846-7555
TELEPHONE: (650) 846-7555
TELEPHONE: GEOU IN NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 34, Application US/08704706A
Patent No. 5958739
GENERAL INFORMATION:
APPLICANT: GENENCOR INTERNATIONAL, INC.
APPLICANT: COLIN MITCHINSON
APPLICANT: ANTHONY G. DAY
APPLICANT: ANNEWS SHAW
TITLE OF INVENTION: MUTANT ALPHA-AMYLASE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Genencor International, Inc. STREET: 925 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
JENCE 483 AA; 55211 MW; 1221290 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 34, Application US/08704706A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 NRVISGEHLIKAWTHFH 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143 VRMIKLDSEKVYWSKRH 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JT 6
US-08-704-706A-34
                                                                                                                                                              STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               XXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 QKGTVRTKYGTKGELQSA-IKSLHSRDINVYGD-VVINHKGGADATEDVTAVEVDP-ADR 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PATENTIN Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,700
FILING DATE:
CLASSIFICATION: 25.2
ATTORNEY/AGENT INFORMATION:
NAME: Stone, Christopher
REGISTRATION NUMBER: 35,696
REFERENCE/DOCKET NUMBER: GC275
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 4.1%; Score 100; DB 1; Length 483; Local Similarity 29.9%; Pred. No. 1.17e+01; es 23; Conservative 21; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          483 AA.
                                                                                                                                                      APPLICANT: COLIN MITCHINSON
APPLICANT: CAROL A. REGNADT
APPLICANT: TRACI H. ROPP
APPLICANT: LEIF P. SOLHEIM
TITLE OF INVENTION: MUTANT ALPHA-AMYLASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International
STREET: 180 Kimball Way
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
HENCE 483 AA; 55211 MW; 1221290 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08914679A
Patent No. 6080568
GENERAL INFORMATION:
APPLICANT: Anthony G. Day
APPLICANT: Barbara A. Swanson
                                                                                                  Sequence 34, Application US/08468700 Patent No. 5736499 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08914679A
                                                             Sequence 34, Application US/08468700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (415) 742-7555
TELEFAX: (415) 742-7515
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 483 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 NRVISGEHLIKAWTHFH 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143 VRMIKLDSEKVYWSKRH 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-914-679A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
```

g

g

CCCCCXEXEXEXCCCCC

```
CLASSIFICATION: 435
                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                      XXXXXX
                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                      RESULT
ID US
                                                                                                                                                                                                                                                                                                                     q
    85555555555555555555555
                                                                                                                                                                                                                                                                                                  ó
                                                                                                                                                                                                                                                                                                                                                                                                      69 QKGTVRTKYGTKGELQSA-IKSLHSRDINVYGD-VVINHKGGADATEDVTAVEVDP-ADR 125
                                                                                                                                                                                                                                                                                                          Score 100; DB 2; Length 483;
Pred. No. 1.17e+01;
21; Mismatches 29; Indels 4; Gaps
                                    CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/704,706A
FILLIG DATE: February 20, 1998
CLASSIFICATION: 455
ATTORNEY,AGENT INFORMATION:
NAME: Stone, Christopher
REGISTRATION NUMBER: 35,696
REFERENCE/DOCKET NUMBER: 35,696
REFERENCE/DOCKET NUMBER: GC275-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 846-7555
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 846-7555
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 846-605
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 483 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 36, Application US/08468698
Patent No. 5849549
GENERAL INFORMATION:
APPLICANT: Barnett, Christopher
APPLICANT: Mitchinson, Colin
APPLICANT: Power, Scott D.
APPLICANT: Solheim, Leif P.
TITLE OF INVENTION: Oxidatively Stable Alpha-Amylase
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,698
FILING DATE: 06-JUN-95
                                                                                                                                                                                                                                                                                                                                                                                                    483 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Genencor International, Inc. STREET: 180 Kimball Way. CITY: South San Francisco STATE: CA
                                                                                                                                                                                                               TOPOLOGY: unknown
MOLECULE TYPE: protein
JENCE 483 AA; 55211 MW; 1221290 CN;
                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 36, Application US/08468698
                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                       SS: single unknown
                                                                                                                                                                                                                                                       Query Match
4.1%;
Best Local Similarity 29.9%;
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                       126 NRVISGEHLIKAWTHFH 142
                                                                                                                                                                                                                                                                                                                                                          143 VRMIKLDSEKVYWSKRH 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                  US-08-468-698-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                        XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                          RESULT
 a
                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                           ò
```

```
69 QKGTVRTKYGTKGELQSA-IKSLHSRDINVYGD-VVINHKGGADATEDVTAVEVDP-ADR 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/08890383
Patent No. 6008026
GENERAL INFORMATION:
APPLICANT: Anthony G. Day
TITLE OF INVENTION: MUTANT ALPHA-AMYLASE HAVING INTRODUCED
TITLE OF INVENTION: THEREIN A DISULFIDE BOND
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 100; DB 2; Length 483;
Pred. No. 1.17e+01;
21; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   483 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Genencor International, Inc. STREET: 925 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/890,383
FILING DATE: TO BE Assigned
ATTORNEY/AGENT INFORMATION:
NAME: Stone, Christopher
REGISTRATION NUMBER: 35,696
REFERNCE/DOCKET NUMBER: GC377
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 846-7555
                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
JENCE 483 AA; 55181 MW; 1222078 CN;
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/194,664
FILING DATE: 10-FEB-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/016,395
FILING DATE: 11-FEB-93
FILING DATE: 11-FEB-93
ATTORNEY/AGENT INFORMATION:
NAME: Stone, Christopher L.
REGISTRATION NUMBER: 35,696
REGISTRATION NUMBER: 35,696
                                                                                                                                                                                                                 GC220D2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/08890383
                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: GCZ
TELECOMMUNICATION INFORMATION:
TELEBHONE: (415) 742-7555
TELEFAX: (415) 742-7217
INFORMATION FOR SEQ ID NO: 36:
                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 483 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                 single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 4.1%;
Local Similarity 29.9%;
les 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 NRVISGEHLIKAWTHFH 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 VRMIKLDSEKVYWSKRH 159
                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 925 Page
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-890-383-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
```

Ŋ

```
69 QKGTVRTKYGTKGELQSA-IKSLHSRDINVYGD-VVINHKGGADATEDVTAVEVDP-ADR 125
                           69 QKGTVRTKYGTKGELQSA-IKSLHSRDINVYGD-VVINHKGGADATEDVTAVEVDP-ADR 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 483;
                                                                                                                                                                                                                                                                                                                                                                                                                              Oxidatively Stable Alpha-Amylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 100; DB 4; Length 483
Pred. No. 1.17e+01;
21; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PATEM: PC-DOS/MS-DOS
SOFTWARE: PATEMIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/01553A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          483 AA.
                                                                                                                                                                                                        483 AA.
                                                                                                                                                                                                                                                                                                                                                             Sequence 36, Application PC/TUS9401553A
GENERAL INFORMATION:
APPLICANT: GENERNCOR INTERNITIONAL, INC.
TITLE OF INVENTION: Oxidatively Stable Alph
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International, Inc.
STREET: 180 Kimball Way
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: HOLD, Margaret A.
REGISTRATION NUMBER: 33,401
REPERBNE/FOCKET NUMBER: GC220-2
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 742-7336
TELEFAX: (415) 742-7217
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 483 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
HRNCE 483 AA; 55181 MW; 1222078 CN;
                                                                                                                                                                                                                                                                                                                             Sequence 36, Application PC/TUS9401553A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 4.1%;
Best Local Similarity 29.9%;
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143 VRMIKLDSEKVYWSKRH 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 NRVISGEHLIKAWTHFH 142
                                                                                  126 .NRVISGEHLIKAWTHFH 142
                                                                                                                          143 VRMIKLDSEKVYWSKRH 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T 11
PCT-US94-01553A-32
                                                                                                                                                                                  T 10
PCT-US94-01553A-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: US ZIP: 94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AXXXX
                                                                                  g
                                                                                                                                                                                                          d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4
                                                                                                                                                                                                                                                                                                           |:| :::||:::||:::|| |:::|| |::|| |:||:::|| |:||:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |::::|| |:::|| |:::|| |:::|| |::::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |::
                                                                                                                                                                                                                                                                                     69 QKGTVRTKYGTKGELQSA-IKSLHSRDINVYGD-VVINHKGGADATEDVTAVEVDP-ADR 125
                                                                                                                                                                                                                                                4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4;
                                                                                                                                                                                                   Score 100; DB 3; Length 483;
Pred. No. 1.17e+01;
21; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 100; DB 4; Length 483;
Pred. No. 1.17e+01;
21; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 32, Application PC/TUS9510426
GENERAL INFORMATION:
APPLICANT: GENEROR INTERNATIONAL, INC.
TITLE OF INVENTION: AN IMPROVED Cleaning Composition
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
OPERATIG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           483 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US95/10426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                           TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
ENCE 483 AA; 55211 MW; 1221290 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: STONE, Christopher L.
REGISTRATION NUMBER: 33,401
REFERENCE/DOCKET NUMBER: GC220-3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 32, Application PC/TUS9510426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (415) 742-7536
TELEFAX: (415) 742-7536
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 180 Kimball Way
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
TELEFAX: (650) 845-6504
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 483 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGIH: 483 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                     Query Match
Best Local Similarity 29.9%;
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 4.1%;
Best Local Similarity 29.9%;
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                   126 NRVISGEHLIKAWTHFH 142
                                                                                                                                                                                                                                                                                                                                                                                                           143 VRMIKLDSEKVYWSKRH 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: US
ZIP: 94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCT-US95-10426-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
ID PC
XX
    8888888888
                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                     a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
```

9

```
126 NRVISGEHLIKAWTHFH 142
                                                                                                                                                                                                                                                                                                                                           143 VRMIKLDSEKVYWSKRH 159
                                                                                 FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CA
USA
                                                                                                                                                                                                    STRANDEDNESS:
          94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94080
                                                                                                                                                                                                                                                                                                                                                                      JT 13
US-08-468-220-32
 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                 XXXXXX
                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                               69 QKGTVRTKYGTKGELQSA-IKSLHSRDINVYGD-VVINHKGGADATEDVTAVEVDP-ADR 125
                                                                                                                                                                                                                                                                                                                                                                                                                            4; Gaps
                                                                                                                                                                                                                                                                                                                                                                           4.1%; Score 100; DB 4; Length 483; 29.9%; Pred. No. 1.17e+01; ative 21; Mismatches 29; Indels
                                 Sequence 32, Application PC/TUS9401553A
GENERAL INFORMATION:
APPLICANT: GENENOR INTERNTIONAL, INC.
TITLE OF INVENTION: Oxidatively Stable Alpha-Amylase
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 36, Application PC/TUS9510426
GENERAL INFORMATION:
APPLICANT: GENERNCOR INTERNATIONAL, INC.
TITLE OF INVENTION: An Improved Cleaning Composition
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International
STREET: 180 Kimball Way
CITY: South San Francisco
STATE: CA
                                                                                                                                                            COMPUTER IS TO COMPUTED SYSTEM: COMPUTED SYSTEM: PC-DOS/WS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/01553A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            483 AA.
                                                                                        ADDRESSEE: Genencor International, Inc.
STREET: 180 Kimball Way
CITY: South San Francisco
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
MENCE 483 AA; 55211 MW; 1221290 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                          GC220-2
                 Sequence 32, Application PC/TUS9401553A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 36, Application PC/TUS9510426
                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Horn, Margaret A.
REGISTRATION UNDRER: 33,401
REFERENCE/DOCKET UNBER: GC22(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 742-7536
TELEFAX: (415) 742-7217
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                LENGIH: 483 amino acids
                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 29.9%;
nes 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    126 NRVISGEHLIKAWTHFH 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143 VRMIKLDSEKVYWSKRH 159
                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                              FILING DATE:
                                                                                                                                     94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCT-US95-10426-36
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             XXXXXX
                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
Q
                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C C C C C C C C C X E X B X B X X X X
```

```
Score 100; DB 4; Length 483;
Pred. No. 1.17e+01;
21; Mismatches 29; Indels 4; Gaps 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 QKGTVRTKYGTKGELQSA-IKSLHSRDINVYGD-VVINHKGGADATEDVTAVEVDP-ADR 125 ·
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Antim, Richard L.
APPLICANT: Barnett, Christopher
APPLICANT: Mitchinson, Colin
APPLICANT: Power, Scott D.
APPLICANT: Requadt, Carol
APPLICANT: Solheim, Leif P.
TITLE OF INVENTION: Oxidatively Stable Alpha-Amylase
CORRESSONDENCES: 68
CORRESSONDENCE ADDRESS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             483 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Genencor International, Inc.
STREET: 180 Kimball Way
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 483 AA; 55181 MW; 1222078 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: GC220-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 742-7536
TELEFAX: (415) 742-7217
INFORMATION FOR SEQ ID NO: 36:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 32, Application US/08468220 Patent No. 5824532 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 32, Application US/08468220
                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: STONE, Christopher L.
REGISTRATION NUMBER: 33,401
                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 483 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 4.1%;
Best Local Similarity 29.9%;
Matches 23; Conservative
```

```
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                 XXXXXX
                                                                                                                                                                                                                                                                                                                                     RESULT
ID PC
                                                                                                                                                                                                                                                                                          ġ
           οχ
                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                               4;
                                                                                                                                                                                                                                                                                  69 QKGTVRTKYGTKGELQSA-IKSLHSRDINVYGD-VVINHKGGADATEDVTAVEVDP-ADR 125
                                                                                                                                                                                                                                  Score 100; DB 2; Length 483;
Pred. No. 1.17e+01;
21; Mismatches 29; Indels 4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 37, Application US/08468220
Patent No. 5824532
GENERAL INFORMATION:
APPLICANT: Barnett, Christopher
APPLICANT: Mitchinson, Colin
APPLICANT: Power, Scott D.
APPLICANT: Solheim, Leif P.
TITLE OF INVENTION: Oxidatively Stable Alpha-Amylase
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC_DOS/MS-DOS
. SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                              487 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genencor International, Inc
APPLICATION NUMBER: US/08/468,220
ELLING DATE: 06-JUN-95
CLASSIFICATION: 435
PRIOR APPLICATION DATE: 08-194,664
FILING DATE: 10-FEB-94
PRIOR APPLICATION DATE: 08-194,664
PRIOR APPLICATION DATE: 08-194,664
PRIOR APPLICATION DATE: 30-FEB-93
ATTONELY AGENT INFORMATION:
NAME: Stone, Christopher L.
REGISTRATION NUMBER: 35,696
REFERNEC/DOCKET NUMBER: GC220D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 742-7555
TELEPHONE: (415) 742-7217
INFORMATION FOR SEQ ID NO: 32:
ELECTHONE CHARACTERISTICS:
LENGTH: 483 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 483 AA; 55211 MW; 1221290 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/468,220 FILING DATE: 06-JUN-95
                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 37, Application US/08468220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 180 Kimball Way
CITY: South San Francisco
STATE: CA
                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                   Query Match
Best Local Similarity 29.9%;
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                          126 NRVISGEHLIKAWTHFH 142
                                                                                                                                                                                                                                                                                                                           143 VRMIKLDSEKVYWSKRH 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                     JT 14
US-08-468-220-37
                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                XXXXXX
                                                                                                                                                                                                                                                                                                                                                     RÈSULT
                                                                                                                                                                                                                                                                                                         g
         8888888888888888888888888888888888
                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                           ò
```

```
73 QKGTVRTKYGTKGELQSA-IKSLHSRDINVYGD-VVINHKGGADATEDVTAVEVDP-ADR 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 37, Application PC/TUS9401553A
GENERAL INFORMATION:
APPLICANT: GENENCOR INTERNITIONAL, INC.
TITLE OF INVENTION: Oxidatively Stable Alpha-Amylase
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International, Inc.
STREET: 180 Kimball Way
CITY: South San Francisco
STAFE: CA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 4.1%; Score 100; DB 2; Length 487; Best Local Similarity 29.9%; Pred. No. 1.17e+01; Matches 23; Conservative 21; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCI/US94/01553A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           487 AA.
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION UNBER: 08/194,664
FILING DATE: 10-FEB-94
PRIOR APPLICATION DATA:
APPLICATION UNBER: 08/016,395
FILING DATE: 11-FEB-93
ATTORNEY/AGENT IRFORMATION:
NAME: Stone, Christopher L.
REGISTRATION NUMBER: 35,696
REFERENCE/DOCKET NUMBER: 35,696
TELECOMMUNICATION INFORMATION:
TELEPAN: (415) 742-7555
TELEPAN: (415) 742-7517
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
TENTH 475 AND AND ACTION OCIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: HOCH, MARGARTA 33,401
REGISTRATION NUMBER: 33,401
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 742-7236
TELEFAX: (415) 742-7236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
JENCE 487 AA; 55495 MW; 1241380 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 37, Application PC/TUS9401553A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 NRVISGEHLIKAWTHFH 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143 VRMIKLDSEKVYWSKRH 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T 15
PCT-US94-01553A-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
```

```
Query Match
4.1%; Score 100; DB 4; Length 487;
Best Local Similarity 29.9%; Pred. No. 1.17e+01;
Matches 23; Conservative 21; Mismatches 29; Indels 4; Gaps
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Innear
MOLECULE TYPE: protein
SEQUENCE 487 AA; 55495 MW; 1241380 CN;
   888888888
```

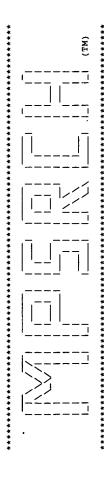
73 QKGTVRTKYGTKGELQSA-IKSLHSRDINVYGD-VVINHKGGADATEDVTAVEVDP-ADR 129 

q

130 NRVISGEHLIKAWTHFH 146 οy q

143 VRMIKLDSEKVYWSKRH 159

Search completed: Thu Aug 24  $18:55:43\ 2000$  Job time :  $27\ secs.$ 



Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Thu Aug 24 18:53:19 2000; MasPar time 18.19 Seconds 850.414 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-214-679-2 (1-328) from US09214679.pep 2417 1 MKWLEESIMAKRGVGAGRKP......GNWVDPKYIVGAMLNKNLLV 328 Title:

Description: Perfect Score:

Sequence:

PAM 150 Gap 11 Scoring table:

142080 seqs, 47172406 residues Searched:

Post-processing: Minimum Match 08 Listing first 45 summaries

pir64 1:pir1 2:pir2 3:pir3 4:pir4 Database:

Mean 48.076; Variance 94.750; scale 0.507 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Pred. No.	1.21e-37	3.15e-27	4.84e-15	1.91e-09	1.69e-08	5.95e-07	3.72e-05	8.78e-01	8.78e-01	6.58e-01	1.55e+00	1.17e+00	1.55e+00	1.17e+00	1.55e+00	2.72e+00	3.60e+00	3.60e+00	2.72e+00	3.60e+00	2.72e+00	3.60e+00	2.06e+00
Description	hypothetical protein	hypothetical protein	probable acetamidase	hypothetical protein	formamidase (EC 3.5.1	acetamidase - Mycobac	probable formamidase	polysialic acid capsu	hypothetical protein	alkylglycerone-phosph	vitamin B12 transport	sensory transduction	hypothetical protein	104K microneme-rhoptr	ryanodine receptor, c	ADP-ribosylation fact	probable formamidase	cell division protein	naringenin-chalcone s	naringenin-chalcone s	capB protein - Bacill	omega-3 fatty acid de	alpha-amylase (EC 3.2
Ωī	E75139	G72414	C72750	E71097	S74213	A47696	T04712	B70434	D70858	JC5829	QRECBC	H69145	A64742	A44945	A37113	C49993	T04713	S73845	T11000	T10951	A30091	T10063	ALBSL
DB	7	~	~	7	~	~	~	-	7	N	П	~	N	N	~	7	~	~	~	~	7	7	7
% Query Match Length DB	298	285	377	389	407	406	432	322	393	597	326	567	810	924	4969	182	307	380	396	396	397	460	512
% Query Match	13.3	11.0	8.2	6.7	6.5	6.1	5.6	4.3	4.3	4.3	4.2	4.2	4.2	4.2	4.2	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.1
Score	322	266	197	1.63	157	147	135	103	103	104	101	102	101	102	101	66	86	86	66	96	66	96	100
Result No.	н	7	m	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23

22 2 MATOIN COMMISSION CHANNET 2	30 4:1 032 2 A4/210 COMPLEMENTALY CILLOMAC 3:	98 4.1 632 2 S27576 rcaC protein - Caloth 3.	99 4.1 4967 2 S72269 ryanodine receptor is 2.	99 4.1 5032 1 A35041 ryanodine receptor ty 2.	99 4.1 5035 1 146646 ryanodine receptor, s	96 4.0 135 2 A48491 twitching motility pr 6.	97 4.0 140 2 B32317 sex-regulated protein 4.	96 4.0 181 2 S49325 ADP-ribosylation fact 6.	96 4.0 181 2 S28875 ADP-ribosylation fact 6	96 4.0 181 2 S66337 ADP-ribosylation fact 6.	97 4.0 252 2 A72708 hypothetical protein 4.	96 4.0 380 2 T06235 omega-3 fatty acid de 6.	96 4.0 396 2 T10961 naringenin-chalcone s 6.	96 4.0 396 2 T10962 naringenin-chalcone s 6.	97 4.0 500 2 C69580 alpha-L-arabinofurano 4.	97 4.0 556 2 E75049 phenylalanyl-tRNA syn 4	97 4.0 638 2 S25767 probable cellulosome 4.	96 4.0 798 2 A69979 conjugation transfer 6.	96 4.0 1249 2 S54376 tripeptidy1-peptidase 6.2	97 4.0 1301 2 S18118 alpha-amylase - Alicy 4.7	97 4.0 1853 2 S33527 cipA protein - Clostr 4.7	5 97 4.0 1854 2 S36859 hypothetical protein 4.7	ALIGNMENTS	1	E/3139 hypothetica	Orsay) RGANISM #formal name Pyrococcus abyssi		E7	LS.	ion submitted to the EMBL Data Library,	Pyrococcus abyssi genome seguence:	. sousakes success tas caseset!	24 98 25 98 26 99 27 99 28 99 29 96 31 96 33 96 33 96 34 97 35 96 36 96 37 96 38 97 41 96 42 97 41 96 42 97 41 96 42 97 41 96 42 97 41 96 42 97 43 97 44 97 45 97 46 97 46 97 46 97 46 97 46 97 46 97 47 97 48 97	# 11 # 11 # 11 # 11 # 11 # 10 # 10	6322 6322 50332 50332 50332 50332 63	22	2 A47210 2 S27576 2 S72569 1 146646 2 A48491 2 B32317 2 S28875 2 S28875 2 S6337 2 T10961 2 T10962 2 T06235 2 T10962 2 T10962 2 S25767 2 A5979 2 S3527 2 S35876 2 S3527 2 S36859 2 S3527 2 S36859 4 LYPE COMPLETE  #TYPE COMPLETE  #TYPE COMPLETE  #TYPE COMPLETE  #TYPE COMPLETE  # SEQUENCE_revise 99 GENOSCOPE 0 the EMBL Data abyssi genome se	amplemed and produced in the product	3.60e+00 2.72e+00 2.72e+00 2.72e+00 6.23e+00 6.23e+00 6.23e+00 6.23e+00 6.23e+00 4.74e+00 4.74e+00 4.74e+00 4.74e+00 4.74e+00 5.23e+00 4.74e+00 5.23e+00 6.23e+00 6.23e+00 6.23e+00 7.74e+
----------------------------------	---	--	---	---	--	--	--	--	---	--	---	--	--	--	--	---	---	---	--	--	--	---	------------	---	-----------------------	--	--	----	-----	---	------------------------------------	---------------------------------	---	--	--	----	---	--	--

RESULT ENTRY TITLE	п	E75139 #type complete hypothetical protein PAB0614 - Pyrococcus abyssi (strain
ORGANISM DATE		Orsay) #formal_name Pyrococcus abyssi 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1000
ACCESSIONS REFERENCE		E75139
#authors	s, s	anonymous, Genoscope
#description	ption	
#accession	ion	E75139
##St	##status	preliminary
### 0E###	##molecule ##residues	##molecule_type DNA ##residnes 1-298 ##label KAW
##CI	oss-ref	##cross-references GB:AJ248285; GB:AL096836; NID:95458067; PIDN:CAR40830 1: PID: 515756: PID:35488341
## ex	perimer	
GENETICS #dene		PAB0614
SUMMARY		#length 298 #molecular-weight 32456 #checksum 8274
Query Matc Best Local Matches	-	Similarity 30.9%; Pred. No. 1.21e-37; 92; Conservative 66; Mismatches 122; Indels 18; Gaps 15;
Db 7	IPRDKHV	IPRDKHVYSFGPNMKEVARAKPGEIVIFQTLDALGGQVKSEEDTIEKI-DFSRVNPATGP 65
Qy 29	: ::   MQKEFH	: ::    ::
99 qa		LYVEGAKRGGILRYD-ILDIKVEGKGAVVTA-PG-AGV-LGKKVERP-QTRICEVK 116
Qy 88	IMVNGA	:  :    :   :    :    :    :    :    :
Db 117	-DGFVI	-DGFVIFKGIKIPAMPMIGVIGVAYD-EEVPTGTPGKHGGNMDTNLIRKGTTIYFPVF 172
Qy 148	LDSEKV	WSKRHTLPYKPHIGTLSVSPEIDSINSLIPDNHGGNMDVPDIGPGSITYPLVR 207
Db 173	VDGAYLA	173 VDGAYLAIGDLHAVMGDGEVCVSACEVSGEVTVRVTPMEG-KLEWPLLETEDSFYLLVSD 231
оу 208	APGGRLE	APGGRLFIGDAHACQGDGBICGTAVEFASITITIKVDLIKNWQLSWPRMENAENIMSIGSA 267
Db 232	ENLDKA	ENLDKAIEEAVSLGVEALRKSNDLS-WDEAYMLASLVMDVEISQLVDPRKTVRVRIPK 288
Qy 268	I: I RPLEDAT	16   1   1   1   1   1   1   1   1   1

N

э;

```
##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               266 NL 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249 QL 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #journal
#title
                                                                                                                                                                                                                                                                                                                                                       4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                         GENETICS
                                               #dene
                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #dene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                               SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARY
                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENTRY
                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DATE
                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                               δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                   #authors Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, E.K.; Peterson, J.D.; Nelson, W.C.; Ketchum, K.A.; McDonald, L.; Utterback, T.R.; Malek, J.A.; Linher, K.D.; Garrett, M.W.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; Heidelberg, J.; Sutton, G.G.; Fleischmann, R.D.; White, O.; Salzberg, S.L.; Smith, H.O.; Venter, J.C.; Fraser, C.M. #title Bacteria from genome sequence of Thermotoga maritima.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##cross-references GB:AE001698; GB:AE000512; NID:g4980609; PID:g4980611; TIGR:TM0119
##experimental_source strain MSB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #authors Rawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.;
Haikawa, Y.; Jin-no, K.; Takahashi, M.; Sekine, M.; Baba,
S.; Ankai, A.; Kosuqi, H.; Hosoyama, A.; Fukui, S.; Nagal,
Y.; Nishijima, K.; Nakazawa, H.; Takamiya, M.; Masuda, S.;
Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.;
Kushida, N.; Oguchi, A.; Aoki, K.; Kubota, K.; Nakamura,
Y.; Nomura, N.; Sako, Y.; Kikuchi, H.

# journal DNA Res. (1999) 6:83-101
# title Complete genome sequence of an aerobic hyper-thermophilic
Crenarchaeon, Aeropyrum pernix K1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C72750 #type complete
probable acetamidase APE0528 - Aeropyrum pernix (strain Kl)
       G72414 #type complete
hypothetical protein TM0119 - Thermotoga maritima (strain
MSB8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 IPIHPMVGVIGVAPQEGEYPTGTAHRHGGNMDTKEI-TENVTVHLPVFQEGALLALGDVH 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              176 ATMGDGEVCVSACEVPAKVVVEIDVSKE-EIKWPVVETNDAYYIIVSLPDIEEALKEVTR 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _name Thermotoga maritima
1999 #sequence_revision 11-Jun-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #formal_name Aeropyrum pernix
20.Aug-1999 #sequence_revision 20-Aug-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #length 285 #molecular-weight 31196 #checksum 8059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            235 ETV-WFIQRRKTIPFTDAYMLASLSVDVGISQLVNPAKTAKARIPKYIF 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 11.0%; Score 266; DB 2; Le Local Similarity 30.8%; Pred. No. 3.15e-27; Nes 52; Conservative 40; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                          1-285 ##label ARN
                                                                                                                                                                                                                                                                                                                                                                                                       preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                preliminary
                                                                         #formal_name TP
11-Jun-1999 #se
11-Jun-1999
G72414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-Aug-1999
C72750
                                                                                                                                                                                                                                                                                                                                                                                                                            ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                     G72414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C72750
                                                                                                                                                                                                                                                                                                                                                                                                                                            ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##residues
                                                                                                                                                                                                                                                                                                                                                                                                           ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##status
                                                                                                                                                                                                                                                                                                                                                                                     #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local §
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           m
                                                                                                                                 ACCESSIONS
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #gene
SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                     PITLE
                   ENTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δλ
```

```
##cross-references GB:AP000004; NID:g3236131; PID:g1031082; PID:g3257456
##experimental_source strain OT3
##note this accession replaces an interim accession for a
sequence replaced by GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hino, Y.; Yamamoto, S.; Sekine, M.; Baba, S.; Kosugi, H.; Hino, Y.; Yamamoto, S.; Sekine, M.; Baba, S.; Kosugi, H.; Hosoyama, A.; Nagai, Y.; Sakai, M.; Ogura, K.; Otsuka, R.; Nakazawa, H.; Takamiya, M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi, A.; Aoki, K.; Yoshizawa, T.; Nakamura, Y.; Robb, F.T.; Horikoshi, K.; Masuchi, Y.; Shizuya, H.; Kikuchi, H. DNA Res. (1998) 5:55-76

Complete sequence and gene organization of the genome of a hyper-thermophilic archaebacterium, Pyrococcus horikoshii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S74213 *type complete formamidase (EC 3.5.1.49) A - Methylophilus methylotrophus formamidase (EC 3.5.1.49) A - Methylophilus methylotrophus 04-Dec-1997 *sequence_revision 12-Dec-1997 *text_change 26-Feb-1998
                                                                                                                                                                                                                                                                                                                           146 LGVMGVAPSKELLKEIKEREDRLLKRGGFVLPPTPEGAVPPREPVASEGLRTIPPRENGG 205
                                                                                                                                                                                                                                                                                                                                                                    206 GHLDVDSVREGAIVIAPVKVEGGGVYAGDAHAMEGDGEVAGHŢTDVTAETTVTVEVIKGL 265
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E71097 #type complete
hypothetical protein PH1041 - Pyrococcus horikoshii
hypothetical Pyrococcus horikoshii
fformal_name Pyrococcus horikoshii
14.Aug-1998 #sequence_revision 14-Aug-1998 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                 206 NLDVRHFSPGSKIYFPVFVEGA-LFSVGDAHYAQGDGEVCGTAIEMGATATLRFGVI 261
##cross-references DDBJ:AP000059; NID:95103911; PIDN:BAA79495.1; PID:d1043281; PID:95104179 ##experimental_source strain K1
                                                                                                                     APE0528
#length 377 #molecular-weight 41052 #checksum 5419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #length 389 #molecular-weight 42005 #checksum 7333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           preliminary; nucleic acid sequence not shown;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                         Score 197; DB 2; Length 377;
Pred. No. 4.84e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 163; DB 2; Length 389
Pred. No. 1.91e-09;
17; Mismatches 21; Indels
                                                                                                                                                                                                                                           Pred. No. 4.84e-15;
27; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1-389 ##label KAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #cross-references MUID:98344137
#accession E71097
                                                                                                                                                                                                         Query Match 8.2%;
Best Local Similarity 34.2%;
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 6.7%;
Best Local Similarity 38.7%;
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S74213; S78115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-Aug-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A71000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PH1041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSIONS
```

ó

1-377 ##label KAW

m

```
#map_position 4 #Introns 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION
                                                                                                                                               #submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##status
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                            #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #journal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208-256
273-321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSIONS
REFERENCE
                                                                       ACCESSIONS
                                                                                                                                                                                                                                                                                                                                                                                                    Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
ORGANISM
                                                                                                                                                                                                                                                                                                             #note
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #gene
 ORGANISM
                                                                                                                                                                                                                                                        GENETICS
                                                                                                                                                                                                                                                                                                                             KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARY
                                                                                                                                                                                                                                                                                                                                              SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
              Wyborn, N.R.; Mills, J.; Williams, S.G.; Jones, C.W.
Eur. J. Biochem. (1996) 240:314-322
Molecular characterisation of formamidase from Methylophilus
                                                                                                                                      ##cross-references EMBL:X99632; NID:g1480104; PID:e256826; PID:g1480105
##cross-references EMBL:X99632; NID:g1480104; PID:e256826; PID:g1480105
##experimental_source strain NCIB 10515
ccession 878115
##molecule_type protein
##residues 1-5;44-47;172-176;211-215 ##label WYC
                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 **REENCE A47696
#authors Mahenthiralingam, E.; Draper, P.; Davis, E.O.; Colston, M.J. #journal J. Gen. Microbiol. (1993) 139:575-583
#title Cloning and sequencing of the gene which encodes the highly inducible acetamidase of Mycobacterium smegmatis.
#cross-references MID:93232774
#contents NTC 8159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##status preliminary
##molecule_type DNA; protein
##residues 1-406 ##label MAH
##residues 1-408 ##label MAH
##residues 1-408 ##label MAH
##residues 1-408 ##label MAH
##note sequence inconsistent with the nucleotide translation sequence extracted from NCBI backbone (NCBIN:129965,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T04712  #type complete
probable formamidase (EC 3.5.1.49) F19F18.40 - Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                    DGARTVPPRENGGNHDIKNFTRGSRIFYP-VFVEGAMLSGGDLHFSQGDGEINFCG-AIE 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           210 EGARTVPPRDHGGNCDIKNLTKGSRVYFPVYVKD-GG-LSMGDLHFSQGDGEITFCG-AI 266
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #text_change
                                                                                                                                                                                                                                                                   fmdA
hydrolase
#length 407 #molecular-weight 44466 #checksum 2787
                                                                                                                                                                                                                                                                                                                                                                                  7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBIP:129966)
#length 406 #molecular-weight 43964 #checksum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 147; DB 2; Length 406; Pred. No. 5.95e-07; 14; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                          Score 157; DB 2; Length 407;
Pred. No. 1.69e-08;
14; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acetamidase - Mycobacterium smegmatis
#formal_name Mycobacterium smegmatis
19-Dec-1993 #sequence_revision 18-Nov-1994
                                                                     methylotrophus.
#cross-references MUID:96439058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 6.1%;
Best Local Similarity 43.8%;
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                          Query Match 6.5%;
Best Local Similarity 45.3%;
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-Mar-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | |: ||| |||:
EFASITTIKVDLIKN 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       267 EMAGYLDIKVGLIKD 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              276 MGGFIDMHVDLIK 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               234 FASITTIKVDLIK 246
                                                                                                                     ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T04712
574213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A47696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A47696
                                                                                                        $74213
                                                                                                                                                                                                  #accession
                                                                                                          #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #accession
                  #authors
#journal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233
                                                      #title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                       #gene
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
DATE
                                                                                                                                                                                                                                                      GENETICS
                                                                                                                                                                                                                                                                                                           SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
```

thaliana

```
B70434 #type complete
polysialic acid capsule expression protein - Aquifex aeolicus
polysialic ancid capsule expression protein - Aquifex aeolicus
10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #superfamily probable ATP-binding protein gutQ; CBS homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 210 EAARTIPGRENGGNCDIKNLSRGSKIYLPVFVEGANLSTGDMHFSQGDGEISFCG-AIEM 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83 GDMGLLDSKDALI-AISNSGESTEVLYVLQYAKALNIPVIGITGNEKSS-LAKYSDVVLK 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Overbeek, R.; Snead, M.A.; Keller, M.; Aujay, M.; Huber, R.; Feldman, R.A.; Short, J.M.; Olson, G.J.; Samson, R.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Bancroft, Mewes, H.W.; Mayer, K.F.X.; Schueller, C. submitted to the Protein Sequence Database, March 1999 T04712
#formal_name Arabidopsis thaliana #common_name mouse-ear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The complete genome of the hyperthermophilic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #length 432 #molecular-weight 47566 #checksum 5561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##residues 1.322 ##label AQF
##cross-references GB:AB000745; NID:92983907; PIDN:AAC07460.1;
##experimental_source strain VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #domain CBS homology #label CBS1\
#domain CBS homology #label CBS2
#length 322 #molecular-weight 35114 #checksum
                                                                                                                                                                                                                                                                             ##residues 1-432 ##label BEV
##cross-references EMBL:AL035605
##experimental_source cultivar Columbia; BAC clone F19F18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                preliminary; nucleic acid sequence translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                            73/3; 153/1; 196/3; 275/2; 356/3; 392/3
F19F18.40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.6%; Score 135; DB 2; Le
Larity 35.6%; Pred. No. 3.72e-05;
Conservative 19; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 8.78e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aquifex aeolicus
#cross-references MUID:98196666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 4.3%;
Best Local Similarity 25.2%;
                                                                        11-Jun-1999
T04712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-Sep-1999
B70434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ::: :|:|
235 ASITTIKVDLIKN 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        269 SGFLELKCEIIRN 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##molecule_type DNA
                                                                                                                                                                                                                                                        ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
nes 26; Conser
                                                                                                                            Z15382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B70434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŏ
```

```
#authors Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.V.; Eiglmeier, R.; Gas, S.; Barry II., C.E.; Tekaia, F.; Badcock, K.; Basham, D.; Brown, D.; Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Harrishy, L.; Jagels, K.; Krogh, A.; McLen, J.; Moule, S.; Murphy, L.; Oliver, S.; Goborne, J.; Onelo, K.; Squres, R.; Sulston, J.E.; Selton, S.; Squres, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

#fournal Nature (1998) 393:537-544
#fitle Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##cross-references GB:AL021287; GB:AL123456; NID:93261508; PID:e123771; PID:92791623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochem. Biophys. Res. Commun. (1998) 242:277-281
Nucleotide sequence of a cDNA clone encoding a Caenorhabditis elegans homolog of mammalian alkyi-dihydroxyacetonephosphate synthase: Evolutionary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4,
                                                                                                                                           D70858 #type complete
hypothetical protein Rv3025c - Mycobacterium tuberculosis
(strain H37RV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 NLAVKGIYWARRDAEPHRRRIVITEVEHHAVLDSVNWLV-EHEGAHVTWLPTAADGSVSA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #active_site Cys (cysteine persulfide intermediate)
#status predicted
#length 393 #molecular-weight 40947 #checksum 4169
                                                                                                                                                                                                           #formal_name Mycobacterium tuberculosis
17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alkyldihydroxyacetonephosphate synthase
#formal_name Caenorhabditis elegans
20-Feb-1998 #sequence_revision 13-Mar-1998 #text_change
JC5829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      de Vet, E.C.J.M.; Prinsen, H.C.M.T.; van den Bosch, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     preliminary; nucleic acid sequence not shown;
                          109 RGVDPYGICAMIPHFGGLTGTDLTAMLNDPLPEKVRMIKLDSEKVYWSKRH 159
141 IPVDR-EACP-F-NLAPTVSSTVTLALGDAIAMTLMKLKGFSQEDF-AKRH 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alkylglycerone-phosphate synthase (EC 2.5.1.26)
Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 103; DB 2; Length 393;
Pred. No. 8.78e-01;
20; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #superfamily nitrogen fixation protein nifs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #type complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##experimental_source strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1-393 ##jabel COL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h 4.3%;
Similarity 25.8%;
17; Conservative
                                                                                                                                                                                                                                                            26-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                           A70500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D70858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JC5829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           204 PLVRAP 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132 TALREA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALTERNATE_NAMES
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #accession
                                                                                                                   σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #journal
#title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #authors
                                                                                                                                                                                                                                                                                  ACCESSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSIONS
                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                 TITLE
                                                                                                                                           SNTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
                                                                                                                                                                                                                                      DATE
셤
                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
```

```
##residues 1-597 ##label DEV
##cross-references GB:AJ002686; NID:92821944; PID:e1248248; PID:92821945
# This enzyme catalyzes the exchange of the acyl chain for a long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.; Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.; Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shāo,
                                                                                                                                                                                                                                                                                                                                5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##residues 1-326 ##label BLAT
##cross-references GB:AE000266; GB:U00096; NID:g1787997;
##cross-references GB:AE000266; GB:U00096; NID:g1787997;
##experimental source strain K-12, substrain MG1655
BNCE
thors Friedrich, M.J.; DeVeaux, L.C.; Kadner, R.J.
Usurnal J. Bacteriol. (1986) 167:928-934
Lie Nucleotide sequence of the blucED genes involved in vitamin B12 transport in Bscherichia coli and homology with components of periplasmic-binding-protein-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                             159 CAIIP-IGG--GTSVTNALDTPETEKRAVISMDMALLDKILWIDRENLTCRAQAGIVGQS 215
                                                                                                                                                                                                                                                                                                                                                                                                    This membrane-associated protein is required for vitamin B12 transport across the cytoplasmic membrane; however, its exact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #authors Rioux, C.R.; Kadner, R.J.
#journal Mol. Gen. Genet. (1989) 217:301-308
#title Vitamin B(12) transport in Escherichia coli K12 does not require the btuE gene of the btuCED operon.
#cross-references MUID:89364713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vitamin B12 transport permease protein btuc precursor - Escherichia coli
#formal_name Escherichia coli
30-Jun-1988 #sequence_revision 05-Dec-1997 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1-110,'LT',113-122,'R',124-285,'DCCWPIL' ##label F. this sequence has been revised in reference S04777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #journal Science (1997) 277:1453-1462
#title The complete genome sequence of Escherichia coli K-12.
#cross-references MUID:97426617
                                                                                                                                                                                                                                #molecular-weight 66559 #checksum 3790
                                                                                                                                                                                                                                                                                                                                7;
                                                                                                                                                                                                                                                                                 Length 597;
                                                                                                                                                                                                                                                       Score 104; DB 2; Length by,
Pred. No. 6.58e-01;
"..matches 29; Indels
#cross-references Witching of peroxisomal targeting signals.
#accession JC5829 #molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #type complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     280-326 ##label RIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             216 LERQLNKKGFTCGHEPDSIEFSTLG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | : : : : | : : : : | 174 PEID-SINSLTPDNHGGNMDVPDIG 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G64929; A24498; S04777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transport systems. #cross-references MUID:86304184
                                                                                                                                                                         chain fatty alcohol.
transferase
#length 597 #mol
                                                                                                                                                                                                                                                                          Query Match
4.3%;
Best Local Similarity 28.2%;
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##molecule_type DNA
##residues 1-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QRECBC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A64720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G64929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S04777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A24498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S04777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #note
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #journal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                   KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                    COMMENT
                                                                                                                                                                                                                             SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENTRY
                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
```

role is not clear.

```
##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #authors
                                                                                                                                                   13
                                                                                                                                                                                                                                                                                                                               #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                           #journal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #journal
                                                                                                                                                                                                                                                                                   ACCESSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #title
                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                              TITLE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENTRY
                                                                                                                                                                          ENTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DATE
                                                                                                                                                                                                                                            DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                         g
                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AG0000
Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.;
Dubois, J.; Aldredge, T.; Bashirzadeh, R.; Blakely, D.;
Cook, R.; Gilbert, K.; Harrison, D.; Hoang, L.; Keaqle, P.;
Lumm, W.; Pothier, B.; Qiu, D.; Spadafora, R.; Vicaire, R.;
Wang, Y.; Wlerzbowski, J.; Gibson, R.; Jiwani, N.; Caruso,
A.; Bush, D.; Safer, H.; Petwell, D.; Prabhakar, S.;
McDougall, S.; Shimer, G.; Goyal, A.; Pietrokovski, S.;
Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##cross-references GB:AE000821; GB:AE000666; NID:g2621414; PID:g2621415 ##experimental_source strain Delta H
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ï
                                                                                                                            #domain signal sequence #status predicted #label SIG\
                                                                                                                                            #product vitamin Bl2 transport permease protein btuc #status predicted #label MAT\
#domain transmembrane #status predicted #label TM01\
#domain transmembrane #status predicted #label TM01\
#domain transmembrane #status predicted #label TM03\
#domain transmembrane #status predicted #label TM03\
#domain transmembrane #status predicted #label TM05\
#domain transmembrane #status predicted #label TM05\
#domain transmembrane #status predicted #label TM05\
#domain transmembrane #status predicted #label TM06\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    454 GVYG-I-HFR-V-DADVRVNLETAIPLGL-LIN-EA--VTNSIRHAFP-SGE-GSITVTM 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             397 IQAMNASEEAREVLRDAQSRVRAMAILH-ET--IYDSGNFTGVDMGSFITRLIERLVSAY 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #69145 #type complete
sensory transduction histidine kinase - Methanobacterium
thermoautotrophicum (strain Delta H)
#formal.name Methanobacterium thermoautotrophicum
05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                      #molecular-weight 34949 #checksum 1332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #length 567 #molecular-weight 62431 #checksum 5446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: functional analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      preliminary; nucleic acid sequence not shown;
                                                           *superfamily vitamin B12 transport protein btuc
transmembrane protein; vitamin B12 transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.2%; Score 102; DB 2; Length 567; 25.2%; Pred. No. 1.17e+00;
                                                                                                                                                                                                                                                                                                                                                                                                             Score 101; DB 1; Length 326;
Pred. No. 1.55e+00;
12; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J.; Reeve, J.N.
J. Bacteriol. (1997) 179:7135-7155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              167 STSVDLRQLMYWMMGGFGGVDWRQSWLMLA 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        comparative genomics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1-567 ##label MTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #cross-references MUID:98037514
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
4.2%;
Best Local Similarity 30.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-Jun-1998
                                                                                                                                                                                                                                                                                                                                             #domain
#length 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##molecule_type DNA
                btuc
37 min
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H69145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MTH356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _
-
..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40;
                                    #map_position
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #start_codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE . #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12
                                                                                                                                                                                                                                                                               190-206
244-260
274-290
305-321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #journal
                                                                                                                                                                                                            90-106
117-133
145-161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSIONS
                                                                                                                                              36-326
                                                                              KEYWORDS
FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #gene
                                                                                                                                                                                          61 - 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARY
                                                                                                                                                                                                                                                                                                                                                                      SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
```

```
Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.; Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.; Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114 LEASGV-RVGESLDRTTIAD-IEKGLE-DFYYSVGKYSASVKAVVTPLPRNRVDLKLVFQ 170-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Iams, K.P.; Young, J.R.; Nene, V.; Desai, J.; Webster, P.; ole-MoiYoi, O.K.; Musoke, A.J.
Mol. Biochem. Parasitol. (1990) 39:47-60
Characterisation of the gene encoding a 104-kilodalton microneme-rhoptry protein of Theileria parva.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            428 GLDNFLVCAWIYVSDGVASL-VHLRIKDRIPANNDIYVLKGD-LYWTRITKIQFTQEIKR 485
115 GICAMIPHFGGLTGTDLTAMLNDPLPEKVRMIKLDSEKVYWSKRHTLPYKPHIGTLSVSP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A44945 #type complete
104K microneme-rhoptry protein - Theileria parva
#formal_name Theileria parva
14-May-1993 #sequence_revision 14-May-1993 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A64742 #type complete
hypothetical protein b0177 - Escherichia coli
#formal_name Escherichia col
12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #title    The complete genome sequence of Escherichia coli K-12
#cross-references MUID:97426617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##molecule_type DNA
##residues 1-92,##label IAM
##cross-references GB:M29954; NID:9161865; PTD:9161866
XY #ength 924 #molecular-weight 103625 #checksum 2611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #checksum 5454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##residues 1-810 ##label BLAT
##cross-references GB:AE000127; GB:U00096; NID:g1786370;
PIDN:AAC73288.1; PID:g1786374; UWGP:b0177
##experimental_source strain K-12, substrain MG1655
FICATION #superfamily protective surface antigen D-15
(X #length 810 #molecular-weight 90552 #checksum 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45; Indels
                                                                                                                                                                                | |:: | :: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: |:: | |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 4.2%; Score 102; DB 2; I Best Local Similarity 22.3%; Pred. No. 1.17e+00; Matches 23; Conservative 30; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 101; DB 2; Pred. No. 1.55e+00;
                                                                                                                   504 ESDGLLYLRVEDDGTGME -- GIPDGTVGLSLMRALADQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science (1997) 277:1453-1462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #cross-references MUID:90158697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 4.2%;
Best Local Similarity 27.1%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-Sep-1997
A44945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   171 EGVSAEIQQI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A64742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 GAINSE-ODI 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A44945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A44945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A64720
```

.. ::

```
Otsu, K.; Willard, H.F.; Khanna, V.K.; Zorzato, F.; Green, N.M.; MacLennan, D.H.
J. Biol. Chem. (1990) 265:13472-13483
Molecular cloning of CDNA encoding the Ca(2+) release channel (ryanodine receptor) of rabbit cardiac muscle sarcoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #superfamily ryanodine receptor; transcription initiation
factor sigma region 1 homology
cardiac muscle; heart; phosphoprotein; transmembrane protein
#length 4969 #molecular-weight 565069 #checksum 5421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       **FERENCE S74212 Nishida, K.; Otsu, K.; Hori, M.; Kuzuya, T.; Tada, M. #authors Nishida, K.; Otsu, K.; Hori, M.; Kuzuya, T.; Tada, M. #iournal Eur J. Biochem. (1996) 240:408-415 Cloning and characterization of the 5'-upstream regulatory region of the Ca2+-release channel gene of cardiac #arcoss-references MuID:96439071 #accession S74212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##residues 1-4969 ##label OTS
##cross-references GB:M59743; GB:J05564; NID:g164831; PIDN:AAA31179.1;
PID:g164832
110 GVDPYGICAMIPHFGGLTGTDLTAMLNDPLPEKVRMIKLDSEKVYWSKRHTLPYKPHIGT 169
                                                                                                                                                                                                                                                                                #formal_name Oryctolagus cuniculus #common_name domestic
rabbit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
4.2%; Score 101; DB 2; Length 4969;
Best Local Similarity 26.6%; Pred. No. 1.55e+00;
Matches 17; Conservative 19; Mismatches 24; Indels 4; Gaps
                                                                                                                                                                                                                                                                                                                                15-Feb-1991 #sequence_revision 15-Feb-1991 #text_change 20-Aug-1999 #37113; S74212 A37113
                                                                                                                                                                                                     A37113 #type complete
ryanodine receptor, cardiac muscle - rabbit
ryanodine receptor 2
                                                                             486 L-VKKSKKKLAPITEEDSDKHDEPPE-GPGASGLP-PKAPGDK 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##residues 1-16 ##label NIS
##cross-references EMBL:X99486; NID:e1000328
##experimental_source strain New Zealand White
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      reticulum.
#cross-references MUID:90337947
#accession A37113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##status preliminary
##molecule_type mRNA
##residues 1-4969 ##lak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##molecule_type_DNA
##residues 1-16
                                                                                                                                                                                                                                                     ALTERNATE_NAMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . #authors
#journal
#title
                                                                                                                                                                                                                                                                                                                                                                                                                                           #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #journal
                                                                                                                                                                                                                                                                                                                                                                                   ACCESSIONS
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENETICS
                                                                                                                                                                           RESULT
ENTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARY
                                                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                                                                      DATE
δλ
                                                  g
```

3386 LKEPTPEAEELFRMVAEVFIYWSKSHN--FKREEQNFVVQNEINNMSFLITDTKS-KMSK 3442

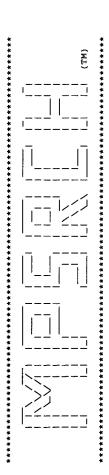
3443 AAVS 3446 : :: 194 PDIG 197

g

oy o

Search completed: Thu Aug 24 18:54:13 2000 Job time : 54 secs.

US-09-214-679-2.rsp



Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Thu Aug 24 18:51:08 2000; MasPar time 11.48 Seconds 885.716 Million cell updates/sec

Tabular output not generated.

Run on:

>US-09-214-679-2 (1-328) from US09214679.pep 2417 1 MKWLEESIWAKRGVGAGRKP......GNMVDPKYTVGAMLNKNLLV 328 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

85661 seqs, 30989116 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

swiss-prot38 1:swissprot Database:

Mean 49.160; Variance 85.522; scale 0.575 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

٠ .	0	ထ	4	Ç	Ţ	_	Ţ	-	Ţ	Ţ	Ţ	o	ō	근	Ō	o	_	_	0	o	0	0	0
Š.	6.09e-10	3.27e-08	.33e-04	2.45e-02	.40e-01	.50e-01	29e-01	50e-01	29e-01	.50e-01	8.38e-01	14e+00	14e+00	38e-01	14e+00	14e+00	8.38e-01	38e-01	08e+00	54e+00	08e+00	2.08e+00	2.08e+00
Pred.	6.0	3.2	1.3	2.4	2.4	4.5	3.2	4.5	3.2	4.5	8.3	1.1	1.1	8.3	1.1	1.1	8.3	8.3	2.0	1.5	2.0	2.0	2.0
ription	FORMAMIDASE (EC 3.5.1.	ACETAMIDASE (EC 3.5.1.	CELL DIVISION PROTEIN	MYOCYTE-SPECIFIC ENHAN	IYPOTHETICAL PROTEIN A	/ITAMIN B12 TRANSPORT	ALPHA-AMYLASE PRECURSO	JNKNOWN PROTEIN FROM 2	104 KDA MICRONEME-RHOP	NYANODINE RECEPTOR, CA	ADP-RIBOSYLATION FACTO	CELL DIVISION PROTEIN	CHALCONE SYNTHASE B (E	CAPB PROTEIN.	OMEGA-3 FATTY ACID DES	RCAC PROTEIN.	RYANODINE RECEPTOR, SK	RYANODINE RECEPTOR, SK	PILG PROTEIN.	SEX-REGULATED PROTEIN	ADP-RIBOSYLATION FACTO	ADP-RIBOSYLATION FACTO	ADP-RIBOSYLATION FACTO
Desc	FOR	ACE	CEL	MYO	HYP	VIT	ALP	UNK	104	RYA	ADP	CEL	CHA	CAP	OME	RCA	RYA	RYA	PIL	SEX	ADP	ADP	ADP
QI	FMDA_METME	AMDA_MYCSM	FTSZ_HALSA	MEFA_MOUSE	YF46_AQUAE	BTUC_ECOLI	AMY_BACLI	UP05_ECOLI	104K_THEPA	RYNC_RABIT	ARF_CRYNE	FTSZ_MYCPN	CHSB_IPOPU	CAPB_BACAN	FD3C_RICCO	RCAC_FREDI	RYNR_HUMAN	RYNR_PIG	PILG_PSEAE	JANB_DROME	ARF1_ARATH	ARF_ORYSA	ARF_MAIZE
DB	н	٦	-	Н	-	7	٦	П	Н	7	7	<b>-</b>	1	П	П	П	٦	П	П	-	٦	7	7
& Query Match Length	407	405	375	498	322	326	.512	810	924	4969	181	380	386	397	460	632	5032	5035	135	140	180	180	180
% Query Match	6.5	6.1	5.2	4.6	4.3	4.2	4.2	4.2	4.2	4.2	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.0	4.0	4.0	4.0	4.0
Score	157	147	125	110	103	101	102	101	102	101	66	86	86	66	86	96	66	66	96	6	96	96	96
Result No.	1	7	m	4	Ŋ	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23

6.5%; Score 157; DB 1; Length 407;

Query Match

2.08e+00	1.54e+00	2.08e+00	1.54e+00	2.81e+00	2.81e+00	2.81e+00	2.81e+00	3.78e+00	2.81e+00	2.81e+00	2.81e+00	6.77e+00	5.06e+00	6.77e+00	5.06e+00	6.77e+00	5.06e+00	5.06e+00	5.06e+00	6.77e+00	6.77e+00
ADP-RIBOSYLATION FACTO	ALPHA-L-ARABINOFURANOS	TRIPEPTIDYL-PEPTIDASE	CELLULOSOMAL SCAFFOLDI	POLYPOROPEPSIN (EC 3.4	CHALCONE SYNTHASE A (E	52 KDA IMMEDIATE-EARLY	OMEGA-3 FATTY ACID DES	PROTEIN YHJJ PRECURSOR	REPLICATION PROTEIN EL	TRIPEPTIDYL-PEPTIDASE	GENOME POLYPROTEIN [CO	ADP-RIBOSYLATION FACTO	ADP-RIBOSYLATION FACTO	FERRITIN LIKE PROTEIN	CHALCONE SYNTHASE B (E	HYPOTHETICAL 41.2 KDA	MUELLERIAN INHIBITING	CELLULOSOMAL SCAFFOLDI	CONTACTIN PRECURSOR (N	SUCROSE-PHOSPHATE SYNT	HYPOTHETICAL 123.9 KDA
ARF1_CHLRE	ABFA_BACSU	TPP2_HUMAN	CIPA_CLOTM	CARP_POLTU	CHSA_IPOPU	IE63_HSVSA	FD3C_ARATH	YHJJ_ECOLI	VE1_HPV09	TPP2_MOUSE	POLG_DEN3	ARF1_DAUCA	ARF_AJECA	FTN1_HAEIN	CHSB_IPOCO	YN28_YEAST	MIS_HUMAN	CIPB_CLOTM	CONT_CHICK	SPS_MAIZE	YEGE_ECOLI
1	Н	1	Н	Н	7	7	-	П	П		7	Н	٦	_	_	٦	Н	Ţ	H	Н	-
180	200	1249	1853	340	396	417	446	498	605	1262	3390	180	182	182	363	373	260	772	1010	1068	1105
4.0	4.0	4.0	4.0	3.9	3.9	3.9	3.9	3.9	3.9	3.9	3.9	3.8	3.8	3.8	3.8	3.8	3.8	3.8	3.8	3.8	3.8
96	97	96	97	92	95	92	92	94	95	95	95	92	93	95	93	92	93	93	93	92	92
24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

#### ALIGNMENTS

| RESOLT<br>ID FMDA_METME STANDARD; PRT; 407 AA.<br>AC 050228: | 050228; | 15-DEC-1998 (Rel. 37, | (Rel. 37,         |   | FORMAMIDASE (EC. 3.5.1.49) (FORMAMIDE AMIDOHYDROLASE)                   | FORMAMILMASE                              |  | _  | Darteria, Drottocharteria, beta embdiricion Metholophilos  | bacteria, Proteobacteria, beta subdivision; metnyiophilus   |  |  | RN [1]   |  |   |   |  | _  |  |   | methy   | Eur.  | [2]  | [7]   | CHARACTERIZATION, AND SEQUENCE OF   |  |  |  
   |   |  |  |  | -  | _  |  | -  | -  | •   
   | +   | <del></del>  |  | This   | +04  | יו ב יוים   
   | the European   | use by   | חחקו ליהח   
   | DOT T TOOM   |   |  
   |   |  |   | Hydrolase.   |  |  
   | SEQUENCE 40/ AA; 44466 MW; |
|--|---------|-----------------------|-------------------|---|---|---|--|--|--|---|--|--|--|--|---|---|--|--|--|---|---|---|--|---|---|--|--
--|---|--|--|--|--|--|--|--
--|---|---|--|--|--
--	---	--
---	--	---
--	---	--
050228		
Jones C.W.; | 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) FORMAMIDASE (EC 3.5.1.49) (FORMAMIDE AMIDOHYDROLASE). FMDA. Methylophilus methylotrophus (Bacterium W3A1). Bacteria; Proteobacteria; beta subdivision; Methylophilus. [1] SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. STRAIN-NCIB 10515; MEDLINE; 96439058. Wyborn N.R., Mills J., Williams S.G., Jones C.W.; "Molecular characteriation of formamidase from Methylophilus methylotrophus."; Eur. J. Blochem. 240:314-322(1996). [2] CHARACTERIZATION, AND SEQUENCE OF 1-5. STRAIN-NCIB 10515; Wyborn N.R., Scherr D.J., Jones C.W.; Wyborn N.R., Scherr D.J., Jones C.W.; "Purification, properties and heterologous expression of formamidase | 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) FORMAMIDASE (EC 3.5.1.49) (FORMAMIDE AMIDOHYDROLASE). FWDA. Methylophilus methylotrophus (Bacterium W3A1). Bacteria; Proteobacteria; beta subdivision; Methylophilus group; Methylophilus. [1] SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. STRANH=NCIB 10515; MEDLINE; 96439058. Wyborn N.R., Mills J., Williams S.G., Jones C.W.; Molecular characterisation of formamidase from Methylophilus methylotrophus. [2] CHARACTERIZATION, AND SEQUENCE OF 1-5. STRAIN=NCIB 10515; Wyborn N.R., Scherr D.J., Jones C.W.; "Putification, properties and heterologous expression of formamidase from Methylophilus methylotrophus."; | 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) FORMAMIDASE (EC 3.5.1.49) (FORMAMIDE AMIDOHYDROLASE). FWDA. Methylophilus methylotrophus (Bacterium W341). Bacteria; Proteobacteria; beta subdivision; Methylophilus group; Methylophilus. [1] SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. STRAIN=NCIB 10515; MEDLINE; 96439058. Wyborn N.R., Mills J., Williams S.G., Jones C.W.; "Molecular characterisation of formamidase from Methylophilus methylotrophus."; Eur. J. Blochem. 240:314-322(1996). [2] CHARACTERIZATION, AND SEQUENCE OF 1-5. STRAIN=NCIB 10515; Wyborn N.R., Scherr D.J., Jones C.W.; FURIfication, properties and heterologous expression of formamidase from Methylophilus methylotrophus."; #Purification, properties and heterologous expression of formamidase from Methylophilus methylotrophus."; #Microbiology 101-194/101-1948. | 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 15-DEC-1998 (Rel. 37, Methylothius group; 16-DEC-1998 (Rel. 37, Methylothius group; 17-DEC-1998 (Rel. 37, Mills J., Williams S.G., Jones C.W.; 18-DEC-1998 (Rel. 314-322(1996)) 16-DEC-1998 (Rel. 314-322(1996)) 17-DEC-1998 (Rel. 37, Jones C.W.; 18-DEC-1998 (Rel. 37, Jone | 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 15-DEC-1998 (Rel. 37, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation update) FORMAMIDASE (EC. 15.1.49) (FORMAMIDE AMIDOHYDROLASE). FORMAMIDASE (EC. 3.5.1.49) (FORMAMIDE AMIDOHYDROLASE). Methylophilus methylotrophus (Bacterium W3Al). Bacteria; Protecobacteria; beta subdivision; Methylophilus group; Methylophilus. [1] SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. STRAIN-NCIB 10515; MODICULE: 96439058. Wyborn N.R., Mills J., Williams S.G., Jones C.W.; "Molecular characterisation of formamidase from Methylophilus methylotrophus."; "Molecular characterisation of formamidase from Methylophilus methylotrophus."; Eur. J. Biochem. 240:314-322(1996). [2] CHARACTERIZATION, AND SEQUENCE OF 1-5. STRAIN-NCIB 10515; Wyborn N.R., Scherr D.J., Jones C.W.; "Purification, properties and heterologous expression of formamidase from Methylothilus methylotrophus."; Microbiology 140:191-195(1994)i- FUNCTION: HYDROLYSE FORMAMIDE WITH THE PRODUCTION OF AMMONIA WHICH | 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) FORMAMIDASE (EC 3.5.1.49) (FORMAMIDE AMIDOHYDROLASE). FORMAMIDASE (EC 3.5.1.49) (FORMAMIDE AMIDOHYDROLASE). Methylophilus methylotrophus (Bacterium W3A1). Bacteria; Proteobacteria; beta subdivision; Methylophilus group; Methylophilus.  [1] SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. STRAIN-NOTED 10515, Wyborn N.R., Mills J., Williams S.G., Jones C.W.; Wyborn N.R., Mills J., Williams S.G., Jones C.W.; Eur. J. Biochem. 240:314-322(1996).  [2] CHARACTERIZATION, AND SEQUENCE OF 1-5. STRAIN-NOIB 10515; Wyborn N.R., Scherr D.J., Jones C.W.; "Purification, properties and heterologous expression of formamidase from Methylophilus methylotrophus."; Microbiology 140:191-195(1994).  -1- FUNCTION: HYDROLYSE FORMAMIDE WITH THE PRODUCTION OF AMMONIA WHICH CAN BE USED AS A SOURCE OF NITROGEN FOR ROWTH. ALSO ACTS, MORE | 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 15-DEC-1998 (Rel. 37, Last asquence update) 15-DEC-1998 (Rel. 37, Last annotation update) FORMAMIDASE (EC 3.5.1.49) (FORMAMIDE AMIDOHYDROLASE). FORMAMIDASE (EC 3.5.1.49) (FORMAMIDE AMIDOHYDROLASE). FORMAMIDASE (EC 3.5.1.49) (FORMAMIDE AMIDOHYDROLASE). Methylophilus methylotrophus (Bacterium W3A1). Bacteria; Proteobacteria; beta subdivision; Methylophilus group; Methylophilus. [1] SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. STRAIN-WCIB 10515; Wyborn N.R., Mills J., Williams S.G., Jones C.W.; Wolocular characterisation of formamidase from Methylophilus methylotrophus."; Wolocular characterise and heterologous expression of formamidase from Methylophilus methylotrophus."; Wyborn N.R., Scherr D.J., Jones C.W.; Wyborn N.R., Scherr D.J., Jones C.W.; Wyborn N.R., Scherr D.J., Jones C.W.; Microbiology 140:191-195(1994)!- FUNCTION: HYDROLYSE FORMAMIDE WITH THE PRODUCTION OF AMMONIA WHICH CAN BE USED AS A SOURCE OF NITROGEN FOR GROWTH. ALSO ACTS, MORE SLOWIX, ON ACETAMIDE, PROPANAMIDE AND BUTANAMIDE. | 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 15-DEC-1998 (Rel. 37, Last asquence update) 15-DEC-1998 (Rel. 37, Last annotation update) FORMAMIDASE (EC 3.5.1.49) (FORMAMIDE AMIDOHYDROLASE). FMDA.  Methylophilus methylotrophus (Bacterium W3A1). Bacteria: Proteobacteria: beta subdivision; Methylophilus group; Methylophilus.  [1] SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. STRAIN-NCIB 10515, MEDLINE; 96439058. Wyborn N.R., Mills J., Williams S.G., Jones C.W.; Myborn N.R., Mills J., Williams S.G., Jones C.W.; Eur. J. Biochem. 240:314-322(1996). [2] CHARACTERIZATION, AND SEQUENCE OF 1-5. STRAIN-NCIB 10515; Wyborn N.R., Scherr D.J., Jones C.W.; "Purification, properties and heterologous expression of formamidase from Methylophilus methylotrophus."; Microlology 140:191-195(1994)i- FUNNTION: HYDROLYSE FORMAMIDE WITH THE PRODUCTION OF AMMONIA WHICH CAN BE USED AS A SOURCE OF NITROGEN FOR GROWTH. ALSO ACTS, MORE SIGNIY. AN ACTERMANDE, PROPANAMIDE AND BETANAMIDE PROPANAMEi- CAN BE USED AS A SOURCE OF NITROGEN FOR GROWTH. ALSO ACTS, MORE SIGNIY, TATC. ACTIVITY: ROPENAMIDE H/230. | 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 15-DEC-1998 (Rel. 37, Last asquence update) 15-DEC-1998 (Rel. 37, Last annotation update) FORMAMIDASE (EC 3.5.1.49) (FORMAMIDE AMIDOHYDROLASE). FURDA.  Methylophilus methylotrophus (Bacterium W3A1). Bacteria; Proteobacteria; beta subdivision; Methylophilus group; Methylophilus. [1] SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. STRAIN-NOIB 10515; Wyborn N.R., Mills J., Williams S.G., Jones C.W.; Molecular characterisation of formamidase from Methylophilus methylotrophus."; Acto:314-322(1996). [2] CHARACTERIZATION, AND SEQUENCE OF 1-5. STRAIN-NOIB 10515; Wyborn N.R., Scherr D.J., Jones C.W.; Wyborn N.R., Scherr D.J., Jones C.W.; Wyborn N.R., Scherr D.J., Jones C.W.; Microbiology 140:191-195(1994)!- FONCTION: HYBOROLYSE FORMAMIDE WITH THE PRODUCTION OF AMMONIA WHICH CAN BE USED AS A SURCE OF NITROGEN FOR GROWTH. ALSO ACTS, MORE SIGMLY, ON ACETAMIDE, PROPANAMIDE AND BUTANAMIDE!- CATALITITY: FORMAMIDE + H(2)O = FORMATE + NH(3). | 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation update) 16-DEC-1998 (Rel. 35.1.49) (FORMAMIDE AMIDOHIDIS group; 17-DEC-1998 (Rel. 36.1.49) (FORMAMIDE C. W.) 18-DEC-1998 (Rel. 36.1.49) (FORMAMIDE AMIDOHIUS group; 18-DEC-1998 (Rel. 30.1.49) | 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 15-DEC-1998 (Rel. 37, Last asquence update) 15-DEC-1998 (Rel. 37, Last annotation update) FORMAMIDASE (Rel. 37, Last annotation update) FORMAMIDASE (EC 3.5.1.49) (FORMAMIDE AMIDOHYDROLASE). FUNDA. Methylophilus methylotrophus (Bacterium W3A1). Bacteria; Proteobacteria; beta subdivision; Methylophilus group; Methylophilus methylotrophus (Bacterium W3A1). SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. STRAIN-NOTB 10515; Wyborn N.R., Mills J., Williams S.G., Jones C.W.; Molecular characterisation of formamidase from Methylophilus methylotrophus.", 240:314-322(1996). [2] CHARACTERIZATION, AND SEQUENCE OF 1-5. STRAIN-NOTB 10515; Wyborn N.R., Scherr D.J., Jones C.W.; Wyborn N.R., Scherr D.J., Jones C.W.; Microbiology 140:191-195(1994) | 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 15-DEC-1998 (Rel. 37, Last asquence update) 15-DEC-1998 (Rel. 37, Last annotation update) FORMAMIDASE (Rel. 35.1.49) (FORMAMIDE AMIDOHYDROLASE). FORMAMIDASE (EC 3.5.1.49) (FORMAMIDE AMIDOHYDROLASE).  Methylophilus methylotrophus (Bacterium W3A1). Bacteria; Proteobacteria; beta subdivision; Methylophilus group; Methylophilus. [1] SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. STRAIN-WCIB 10515; Wyborn N.R., Mills 3., Williams S.G., Jones C.W.; Wyborn N.R., Mills 3., Williams S.G., Jones C.W.; Molecular characterisation of formamidase from Methylophilus methylotrophus."; "Molecular characterisation of formamidase from Methylophilus methylotrophus."; "Wyborn N.R., Scherr D.J., Jones C.W.; "Purification, properties and heterologous expression of formamidase from Methylophilus methylotrophus."; "Mulcrobiology 140:191-195(1994)! FUNCTION: HYDROLYSE FORMAMIDE AND BUTANAMEDE! CATALYTIC ACTIVITY: FORMAMIDE AH (2)0 = FORMATE + NH(3)! CATALYTIC ACTIVITY: FORMAMIDE + H(2)0 = FORMATE + NH(3)! SUBUNIT: HOMOFRENEY: WM=44481; WM_ERR=26; METHOD=ELECTROSPRAY! SUBUNITY: STRONG; TO
M. SMEGRAFIS ACETAMIDASE. | 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 15-DEC-1998 (Rel. 37, Last asquence update) 15-DEC-1998 (Rel. 37, Last annotation update) FORMAMIDASE (EC 3.5.1.49) (FORMAMIDE AMIDOHYDROLASE). FURDAL FURDAL METHYLOPHIUS METHYLOTROPHUS (Bacterium W3A1). Bacteria; Proteobacteria; beta subdivision; Methylophilus group; Methylophilus. [1] SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. STRAIN-NOTED 10515; Wyborn N.R., Mills J., Williams S.G., Jones C.W.; Wyborn N.R., Mills J., Williams S.G., Jones C.W.; Wyborn N.R., Mills J., Williams S.G., Jones C.W.; FULL J. Biochem. 240:314-322(1996). [2] CHARACTERIZATION, AND SEQUENCE OF 1-5. STRAIN-NOIED 10515; Wyborn N.R., Schert D.J., Jones C.W.; Purification, properties and heterologous expression of formamidase from Methylophilus methylotrophus.; MICTOBIOLOGY 140:191-195(1994) | 15-DB<br>15-DB<br>15-DB<br>FORMA<br>Methy,<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy | 15-DB<br>15-DB<br>15-DB<br>15-DB<br>15-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB<br>16-DB |
15-DB<br>15-DB<br>15-DB<br>FORMA<br>Methy,<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy<br>Methy | 15-DB<br>15-DB<br>15-DB<br>15-DB<br>15-DB<br>Methly<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos | 15-DB<br>15-DB<br>15-DB<br>FFORM<br>Methy,<br>Methy<br>Methy<br>Mole<br>Methy<br>Mybou<br>Wybou<br>Wybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou |
15-DB<br>15-DB<br>15-DB<br>15-DB<br>15-DB<br>Methy,<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos | 15-DB<br>15-DB<br>15-DB<br>FORMA<br>Methy,<br>Methy<br>Methy<br>Molt<br>Molt<br>Mybou<br>Wybou<br>Wybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>M | 15-DB<br>15-DB<br>15-DB<br>15-DB<br>15-DB<br>Methly<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos<br>Mybos |
15-DB<br>15-DB<br>15-DB<br>FORMA<br>Methy,<br>Methy,<br>Methy<br>Molt<br>Molt<br>Mybou<br>Wybou<br>Wybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou | 15-DB<br>15-DB<br>15-DB<br>15-DB<br>15-DB<br>Methly<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou | 15-DB<br>15-DB<br>FORMA<br>Methya<br>Methya<br>Methya<br>Mybon<br>Wybon<br>Wybon<br>Wybon<br>Mybon<br>Mybon<br>Mybon<br>Mybon<br>Mybon<br>Mybon<br>Tlan<br>from<br>from<br>from<br>from<br>from<br>from<br>from<br>from | 15-DB<br>15-DB<br>15-DB<br>15-DB<br>FORMA<br>Methyl<br>Bacthy<br>Bacthy<br>Bacthy<br>Wybon<br>Wybon<br>Wybon<br>Wybon<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Flour<br>Fl | 15-DB<br>15-DB<br>15-DB<br>FORM<br>Methya<br>Methya<br>Mybon<br>Wybon<br>Wybon<br>Wybon<br>Mybon<br>Mybon<br>Mybon<br>Mybon<br>Mybon<br>Mybon<br>Flan<br>Flan<br>Flan<br>Flan<br>Flan<br>Flan<br>Flan<br>Fla |
15-DB<br>15-DB<br>15-DB<br>15-DB<br>15-DB<br>Methly<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou<br>Mybou |                            |

```
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LT 4
MEFA_MOUSE
Q60929;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEF2A.
   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifited and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
             é
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4;
                                                                                                                                                                                                                                                                                                       Mahenthiralingam E., Draper P., Davis B.O., Colston M.J.;
"Cloning and sequencing of the gene which encodes the highly inducible acetamidase of Mycobacterium smegmatis.";
J. Gen. Microbiol. 139:575-583(1993)
-1- FUNCTION: ALLOWS ACETAMIDE TO BE USED AS A SOLE CARBON OR NITROGEN
                                  210 EGARTVPPRDHGGNCDIKNLTKGSRVYFPVYVKD-GG-LSMGDLHFSQGDGEITFCG-AI 266
                                               217 DGARTVPPRENGGNHDIKNFTRGSRIFYP-VFVEGAMLSGGDLHFSQGDGEINFCG-AIE 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |: :: | ::||| |: :: || || || |: |
177 DSINSLIPDNHGGNMDVPDIGPGS-1TYPLVRAPGGRLFIGDAHACQGDGEI--CGTAVE 233
            Gaps
                                                                                                                                                                                                                                                  Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.
                                                                                                                                                                                                                                                           [1]
SEQUENCE FROM N.A., AND SEQUENCE OF 1-23; 81-100 AND 180-194.
STRAIN-NCTC 8159;
MEDLINE; 93232774.
                                                                                                                                                                                                                                                                                                                                                                  SOURCE.
-!- CATALYTIC ACTIVITY: FORMAMIDE + H(2)O = FORMATE + NH(3).
-!- SIMILARITY: STRONG, TO M.METHYLOTROPHUS FORMAMIDASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
Halobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 405;
             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14; Mismatches 22; Indels
                                                                                                                                                                                                                                     Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
05E2E359210E0BF2 CRC64;
 Pred. No. 6.09e-10;
14; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 147; DB 1;
Pred. No. 3.27e-08;
                                                                                                                                                                          (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 37, Last annotation update)
(EC 3.5.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15.FEB-2000 (Rel. 39, Last annotation update)
CELL DIVISION PROFEIN FTSZ HOMOLOG.
                                                                                                                                                     405 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      375 AA
                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               405 AA; 43833 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X57175; CAA40462.1; -.
Best Local Similarity 45.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 6.1%;
Local Similarity 43.8%;
            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                              | |: ||| |||:
233 EFASITTIKVDLIKN 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Halobacterium salinarium.
                                                                              267 EMAGYLDIKVGLIKD 281
                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                          Mycobacterium smegmatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 234 FASITTIKVDLIK 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 275 MGGFIDMHVDLIK 287
                                                                                                                                                                          01-NOV-1995
01-NOV-1995
                                                                                                                                                                                                              ACETAMIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FTSZ_HALSA
Q48290;
                                                                                                                                         T 2
AMDA_MYCSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INIT_MET
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                  007838;
           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                         RESULT
                                  a
                                                                              g
                                                                                                                                                     ô
                                                                                                      δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ω,
MEDLINE; 96200101.

Margolin W., Wang R., Kumar M.;

J. Bacterion of an fits homolog from the evolution of Fts2 and tubulin.";

J. Bacteriol. 178:1320-1327(1996).

J. Bacteriol. 178:1320-1327(1996).

ITS SEEMS TO ASSEMBLE INTO A DYNAMIC RING ON THE INNER SURFACE OF THE CYTOPLASMIC AND THE PLACE WHERE DIVISION WILL OCCUR, AND THE FORMATION OF THE RING IS THE SIGNAL FOR SEPTATION TO BEGIN. BINDS TO AND HYDROLYSES GTP (BY SIMILARITY).

-1- SUBUNIT: AGGREGATE TO FORM A RING-LIKE STRUCTURE (BY SIMILARITY).

-1- SIMILARITY: BELONGS TO THE FTSZ FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     186 DQIIAETVKGISETITQPSLINLDYADMTAIMNQGGVAVMLVGETQDKNKTNEVVKDAMN 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 246 HPLLDVDYRGASGGLVHITG--GPDLTLKEAEGIADNI-TERLDASANVIWGARIQESYK 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The expression of MEF2 genes is implicated in CNS neuronal differentiation.";

"The expression of MEF2 genes is implicated in CNS neuronal differentiation.";

Brain Res. Mol. Brain Res. 42:307-316(1996).

-!- FUNCTION: TRANSCRIPTION FACTOR WHICH BINDS SPECIFICALLY TO THE MEP2 ELEMENT IN THE REGULATORY REGIONS OF MANY MUSCLESSPECIFIC GENES. ACTIVATES TRANSCRIPTION VIA THIS ELEMENT. MAY BE INVOLVED IN MUSCLE-SPECIFIC AND/OR GROWTH FACTOR-RELAID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 1.33e-04;
35; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSLED; FOALTON, ...___, CELL division; Septation; GTP-binding.
NP_BIND 105 113 GTP (POTENTIAL).
FEATHBRING 375 AA: 39261 MW; 43A05013AB3E5BEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 125; DB x,
NO. 1.33e-04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-DEC-1998 (Rel. 37, Last annotation update)
MYOCYTE-SPECIFIC ENHANCER FACTOR 2A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         498 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        303 GKVRVMAIMTGVQSAQVLGPSTQ 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          165 PHIGTLSVSPEIDSINSLTPDNH 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP, Q57816, 1FSZ.

PFAM: PF00091; tubulin: 1.

PRINTS; PR00423; CELLDVISFTSZ.

PROSITE; PS01134; FTSZ_1: 1.

PROSITE; PS01135; FTSZ_2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata; C
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U32860; AAB06191.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 5.2%;
Best Local Similarity 23.8%;
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-CEREBELLUM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 97165895
```

m

g

a ö

ď

```
7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=K12;
Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Horiuchi T.,
Ikemoto K., Inada T., Isono K., Isono S., Itoh T., Kanai K., Kasai H.,
Kashimoto K., Kim S., Kimura S., Kitagawa M., Kitakawa M., Makino K.,
Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y.,
Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y.,
Masuda C., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y.,
Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
-- FOWTION: PART OF THE BINDING-PROYEIN-DEPENDENT TRANSPORT SYSTEM
FOR VITAMIN B12. PROBABLY RESPONSIBLE FOR THE TRANSLOCATION OF THE
SUBSTRAITE ACROSS THE MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GDMGLLDSKDALI-AISNSGESTEVLYVLQYAKALNIPVIGITGNEKSS-LAKYSDVVLK 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50 GDRIIVDTRDAFEGAINSEQDIPSQLLKMPFLNPQNGPIM-VNGAEKGDVLAVYIESMLP 108
                                                                                                                                                                                                                                                                                                            Score 103; DB 1; Length 322;
Pred. No. 2.40e-01;
35; Mismatches 41; Indels 7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 89364713.
Rioux C.R., Kadner R.J.;
"Vitamin B12 transport in Bscherichia coli K12 does not require the butting ene of the btucke operon.";
Mol. Gen. Genet. 217:301-308(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner F.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Friedrich M.J., Deveaux L.C., Kadner R.J.;
"Nucleotide sequence of the btuCED genes involved in vitamin B12
transport in Escherichia coli and homology with components of
periplasmic-binding-protein-dependent transport systems.";
J. Bacteriol. 167:928-934(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 IPVDR-EACP-F-NLAPTVSSTVTLALGDAIAMTLMKLKGFSQEDF-AKRH 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 RGVDPYGICAMIPHFGGLTGTDLTAMLNDPLPEKVRMIKLDSEKVYWSKRH 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                            74BE86D9B8FB2A69 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRUC_ECOLI STANDARD; PRT; 326 AA.
P06609; P77197;
01-JAN-1988 (Rel. 06, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
VITAMIN B12 TRANSPORT SYSTEM PERMEASE PROTEIN BTUC.
                                                                                                                                         (POTENTIAL)
                                                                                                          ATP-binding;
                                                                                                                                      ATP
                                                                                                                                                                                                                CBS
321 C
35114 MW;
                                                                                                                                                                                                                                                                                                            y Match 4.3%;
Local Similarity 25.2%;
hes 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
```

```
MEDLINE; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACT_SITE
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best
     RRITTTTTTTTTTTTTS
                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yuuki T., Nomura T., Tezuka H., Tsuboi A., Yamagata H., Tsukagoshi N., Udaka S.;
"Complete nucleotide sequence of a gene coding for heat- and PH-stable alpha-amylase of Bacillus licheniformis: comparison of the amino acid sequences of three bacterial liquefying alpha-amylases
 SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                    SIMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-
                              PROTEIN-DEPENDENT TRANSPORT SYSTEMS. BELONGS TO THE FECCD
                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                            PRAM; PF01032; FecCD_family; 1.
PROSITE; PS00402; BPD_TRANSP_INN_MEMBR; FALSE_NEG.
Cobalt transport; Transport; Transmembrane; Inner membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gray G.L., Mainzer S.E., Rey M.W., Lamsa M.H., Kindle K.L.,
                                                                                                                                                                                                                                                                                                                                                                          Length 326;
                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 4.50e-01;
12; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JAN-1988 (Rel. 06, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
ALPHA-AMYLASE PRECURSOR (EC 3.2.1.1) (1,4-ALPHA-D-GLUCAN
                                                                                                                                                                                                                                                                                                                                              -> R (IN REF. 1).
C65882B1C47BFE69 CRC64;
                                                                                                                                                                                                                                                                                                                                  QL -> LT (IN REF. 1).
A -> R (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                              POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                               167 STSVDLRQLMYWMMGGFGGVDWRQSWLMLA 196
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 101;
                                                                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          luced from the DNA sequences.";
Biochem. 98:1147-1156(1985).
                                                                                                                                        EMBL; M14031; AAA23526.1; -.
EMBL; BA000266; AAC74781.1; -.
EMBL; D90814; CAB21413.1; -.
EMBL; D90813; CAB21399.1; -.
PIR; A4498; ORECBC.
PIR; S04777; S04777.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last seq
                                                                                                                                                                                                                                                                                                                                                      MW;
                                                                                                                                                                                                                                                                                                                                                                        4.2%;
                                                                                                                                                                                                                                                                                                                                                      34949
                                                                                                                                                                                                                                                                                                                                                                                            9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AMYS OR AMYL.
Bacillus licheniformis.
                                                                                                                                                                                                                                                                       133
166
204
260
294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN=ATCC 27811; MEDLINE; 86111694.
                                                                                                                                                                                                                                                                                                                                                    326 AA;
                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLUCANOHYDROLASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 86195857.
            (POTENTIAL).
                                         SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AMY_BACLI
P06278;
                                                                                                                                                                                                                                                                                         TRANSMEM
TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                TRANSMEM
                                                                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            deduced
                                                                                                                                                                                                                                                                                                                                                                                            Aatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
a
a
                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A00844; ALBSL.
PIR; B24549; B34549.
PIR; B24549; A26151.
PIR; A26151; A26151.
PDB; 1BPL; 17-AUG-96.
PDB; 1VJS; 12-MAR-97.
PFAM; PF00128; alpha-amylase; 1.
Hydrolase; Glycosidase; Carbohydrate metabolism; Signal; 3D-structure. SIGNAL
                                                                                                                                                                                              Stephens M.A., Ortlepp S.A., Ollington J.F., McConnell D.J.; "Nucleotide sequence of the 5' region of the Bacillus licheniformis alpha-amylase gene: comparison with the B. amyloliquefaciens gene."; J. Bacteriol. 158:369-372(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=ATCC 27811;
MEDLINE; 95182462.
Machius M., Wiegand G., Huber R.;
"Crystal structure of calcium-depleted Bacillus licheniformis alpha-
                                                                                                                                                                                                                                                                                                                                                                                             Laoide B.M., Chambliss G.H., McConnell D.J.; Bacillus licheniformis alpha-amylase gene, amyL, is subject to promoter-independent catabolite repression in Bacillus subtilis."; J. Bacteriol. 171:243-2442(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amylase at 2.2-A resolution.";
J. Mol. Biol. 246:545-559(1995).
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.
-!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 82098050.

Kuhn H., Fietzek P.P., Lampen J.O.;

"N-terminal amino acid sequence of Bacillus licheniformis alpha-amylases: comparison with Bacillus amyloliquefaciens and Bacillus subtilis Enzymes.";

J. Bacteriol. 149:372-373(1982).
                                      οŧ
Carmona C., Requadt C.;
Structural genes encoding the thermophilic alpha-amylases
Bacillus stearothermophius and Bacillus licheniformis.";
J. Bacteriol. 166:635-643(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALPHA-AMYLASE.
BY SIMILARITY.
BY SIMILARITY.
Q -> Y (IN REF. 5).
R -> L (IN REF. 2).
S -> G (IN REF. 2).
A -> S (IN REF. 2).
A -> S (IN REF. 2).
W, D8BB77759CD4C4482 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 102; DB 1;
Pred. No. 3.29e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58549 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X03236; CAA26981.1; -. EMBL; M38570; AAA22226.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M13256; AAA22240.1; -- EMBL; K01984; AAA22193.1; -- EMBL; M26412; AAA22237.1; -- EMBL; A17930; CAA01355.1; --
                                                                                                                                         SEQUENCE OF 1-104 FROM N.A.
                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-29 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29
512
260
264
357
339
339
                                                                                                                                                                                                                                                                                                                                                                            89213924.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 512 AA;
                                                                                                                                                                          84185455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 30-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30
2260
2264
357
38
38
339
349
```

Matches

셤

g ò

ò

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    428 GLDNFLVCAWIYVSDGVASL-VHLRIKDRIPANNDIYVLKGD-LYWTRITKIQFTQEIKR 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114 LEASGV-RVGESLDRTTIAD-IEKGLE-DFYYSVGKYSASVKAVVTPLPRNRVDLKLVFQ 170
                                       "Characterisation of the gene encoding a 104-kilodalton microneme-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                              01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-AGG-1992 (Rel. 23, Last annotation update)
104 KDA MICRONEME-RHOPTRY ANTIGEN.
Theileria parva.
Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theilerlidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 102; DB 1; Length 924;
Pred. No. 3.29e-01;
30; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rhoptry protein of Theileria parva.";

Mol. Biochem. Parasitol. 39:47-60(1990).
-!- SUBCELLULAR LOCATION: IN MICRONEME/RHOPTRY COMPLEXES.
-!- DEVELOPMENTAL STAGE: SPOROZOITE ANTIGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     905 924 HYDROPHOBIC.
924 AA; 103625 MW; 289B4B554A61870E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=MUGUGA;
MEDLINE; 90158697.

Iams K.P., Young J.R., Nene V., Desai J., Webster P.,
Ole-Moiyoi O.K., Musoke A.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   486 L-VKKSKKKLAPITEEDSDKHDEPPE-GPGASGLP-PKAPGDK 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                         924 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 4969 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYDROPHOBIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RYANODINE RECEPTOR, CARDIAC MUSCLE.
                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M29954; AAA18217.1; -. PIR; A44945.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antigen; Sporozoite; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 22.3%;
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE=HEART MUSCLE;
                                                                                                                              171 EGVSAEIQQI 180
                                                                                                                                                                   ::::| |:|
63 GAINSE-QDI 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RYNC_RABIT
                                                                                                                                                                                                                                                                                                                         104K_THEPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Theileria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P30957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
DE RY
DAC P3
AC P3
DT 01
DT 01
DD 01
DD CO
CC EU
CC E
                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                  òγ
                                                                                                                           a
                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
      4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5,
                                                                                                QKGTVRTKYGTKGELQSA-IKSLHSRDINVYGD-VVINHKGGADATEDVTAVEVDP-ADR 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Link A.J., Robison K., Church G.M.; "Comparing the predicted and observed properties of proteins encoded in the genome of Escherichia coli K-12."; Electrophoresis 18:1259-1313(1997).
-i- SIMILARITY: STRONG, TO H.INFLUENZAE PROTECTIVE SURFACE ANTIGEN D15.
      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-KIZ, MG1655;
MEDLINE; 97426617.
MEDLINE; 97426617.
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner F.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., "The complete genome sequence of Escherichia coll K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Schramm S., Duncan M., Allen E., Araujo R., Aparicio A., Chung E., Davis K., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lashkari D., Lew H., Lin D., Namath A., Oefner P., Roberts D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UNKNOWN PROTEIN FROM 2D-PAGE SPOTS M62/M63/03/09/T35.
DDCE4C6D341664EB CRC64;
                                                                                                                                                                                                                                                                                                                                                JT 8

1005_ECOLI STANDARD, PRT; 810 AA.

P39170; P39181; P77465;

01-FEB-1995 (Rel. 31, Created)

01-NOV-1997 (Rel. 35, Last sequence update)

15-FEB-2000 (Rel. 39, Last annotation update)

UNKNOWN PROTEIN FROM 2D-PAGE SPOTS M62/M63/03/09/735 PRECURSOR.
   4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 101; DB 1; Length 810;
Pred. No. 4.50e-01;
22; Mismatches 24; Indels
21; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFAM; PF01103; Bac_surface_Ag; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE000127; AAC73288.1; -.
EMBL; U70214; AAB08606.1; -.
SWISS-2DPAGE; P39170; COLI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 21-32 AND 351-362.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               810 AA; 90552 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 4.2%;
Best Local Similarity 27.1%;
Matches 19; Conservative
                                                                                                                                                                                          155 NRVISGEHRIKAWTHFH 171
                                                                                                                                                                                                                                                   143 VRMIKLDSEKVYWSKRH 159
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20
810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ECOGENE; EG12676; YAET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=K12 / EMG2;
MEDLINE; 97443975.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1
```

ŝ

Š

SEQUENCE

Signal. SIGNAL

```
qq
                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce.or send an email to license@isb-sib.ch).
                                                                                                                                                                 SARCOPLASMIC RETUCLION DELIMENTATANSVERSE TUDBULES AND
SARCOPLASMIC RETUCLION DELIMENTATANSVERSE TUDBULES AND
BY RELEASE OF CA++ FROM SR FOLLOWING DEPOLARIZATION OF T-TUBBULES.
-! SUBBUIT: HOMOTETRAMER (POTENTIAL).
-! TISSUE SPECIFICITY: HEART AND BRAIN.
-! MISCELLANEOUS: THE CALCIUM RELEASE CHANNEL IS MODULATED BY CA++,
MAY, AND CALMODULIN.
-! MISCELLANEOUS: THE CALCIUM RELEASE CHANNEL ACTIVITY RESIDES IN THE
C-TERMINAL REGION WHILE THE REMAINING PART OF THE PROTEIN
CONSTITUTES THE 'FOOT' STRUCTURE SPANNING THE JUNCTIONAL GAP
BETWEEN THE SR AND THE T-TUBBULE. IT IS POSSIBLE THAT THE FOOT
STRUCTURE INTERACTS WITH THE CYTOPLASMIC REGION OF THE
                                                                                                                                                                                                                                                                                                        MISCELLANEOUS: RYANDDINE IS AN ALKALOID THAT BINDS TO THE CARELEASE CHANNEL IN JUNCTIONAL SR AND MODULATES ITS ACTIVITY. SIMILARITY: LOCAL & LOW WITH THE NICOTINIC ACETYLCHOLINE RECEPTOR (N-ACHR) SUBUNITS.
                                                                                                             Witcher D.R., Kovacs R.J., Schulman H., Cefali D.C., Jones L.R., "Unique phosphorylation site on the cardiac ryanodine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Receptor; Transmembrane; Ionic channel; Calcium channel; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CALMODULIN (POTENTIAL).
CALMODULIN (POTENTIAL).
CALMODULIN (POTENTIAL).
PHOSPHORYLATION (BY CAM-KINASE).
                                 "Molecular cloning of cDNA encoding the Ca2+ release channel (ryanodine receptor) of rabbit cardiac muscle sarcoplasmic
          Otsu K., Willard H.F., Khanna V.K., Zorzato F., Green N.M.,
                                                                                                                                    regulates calcium channel activity.",
J. Biol. Chem. 266:11144-11152(1991).
-!- FUNCTION: COMMUNICATION BETWEEN TRANSVERSE-TUBULES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MW; FF6E0684B974BB4D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
APPROXIMATE REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MODULATOR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                  J. Biol. Chem. 265:13472-13483(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phosphorylation; Glycoprotein.
DOMAIN 1 3090 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A37113; A37113.
PFAM; PF01365; RYDR_ITPR; 1.
PFAM; PF00622; SPRY; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M59743; AAA31179.1; -.
                                                                                        PHOSPHORYLATION OF SER-2809. MEDLINE; 91250425.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PR00795; RYANODINER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      565060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2926
3016
2807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4752
4788
4829
4869
2926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             966
1080
2811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4257
                       Maclennan D.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4105
4796
4969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3941
                                                        reticulum.
                                                                                                   MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEM
TRANSMEM
TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BINDING
MOD_RES
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPEAT
                                                                                                                                                                                                                                                                                                                                +
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                            Gaps 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ς,
                                                                         3386 LKEPTPEAEELFRMVAEVFIYWSKSHN--FKREEQNFVVQNEINNMSFLITDTKS-KMSK 3442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88 IFVVDSNDRERITEAREELQRML-SEDELRDALL-LVFANKQDLPNAMNAAEITDKLGL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Gaps
                                          4;
                                                                                                                                                                                                                                                                                                                                                                                                            Basidiomycota; Hymenomycetes; Tremellales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM; PF00025; arf; 1.
PROSITE; PS01019; ARF; 1.
GTP-binding; Multigene family; Myristate; Protein transport;
Score 101; DB 1; Length 4969;
Pred. No. 4.50e-01;
19; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
C7A9217BECB18A84 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                         Cryptococcus neoformans (Filobasidiella neoformans)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 99; DB 1; L
Pred. No. 8.38e-01;
                                                                                                                                                                                                                                                                                          01-FEB-1994 (Rel. 28, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    380 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND MYRISTOYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MYRISTATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
1
3 30
70
128
20461 MW; C.
4.19
                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Fungi, Basidiomyco
Tremellaceae, Filobasidiella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L25115; AAA17546.1; -. HSSP; P32889; 1RRF.
 Query Match 4.2%;
Best Local Similarity 26.6%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.1%;
28.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17; Conservative
                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                    ADP-RIBOSYLATION FACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-L210425;
                                                                                                                                                3443 AAVS 3446
                                                                                                                                                                       : : :
194 PDIG 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Golgi stack.
INIT_MET
LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
ID FTSZ_MYCPN
AC P75464;
                                                                                                                                                                                                                                                          ARF_CRYNE P34728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ON BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
```

```
PIR; A30091; A30091.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P19580;
  유
                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ä
                                                                                                                                                                                                                       -i - FUNCTION: THIS PROTEIN IS ESSENTIAL TO THE CELL-DIVISION PROCESS.

ITS SEEMS TO ASSENBLE INTO A DYNAMIC RING ON THE INNER SUBRACE OF THE CYTOPLASMIC MEMBRANE AT THE PLACE WHERE DIVISION WILL OCCUR, AND THE FORMATION OF THE RING IS THE SIGNAL FOR SEPTATION TO BEGIN. BINDS TO AND HYDROLYZES GTP (BY SIMILARITY).

-i SUBGELLULAR LOCATION: CYTOPLASMIC. ASSEMBLE AT THE INNER SURFACE OF THE CYTOPLASMIC MEMBRANE (BY SIMILARITY).

-i SUBCELLULAR LOCATION: CYTOPLASMIC. ASSEMBLE AT THE INNER SURFACE -: SIMILARITY: BELONGS TO THE FTSZ FAMILY.
                                                                                                                                                                                  Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ipomoea purpurea (Common morning-glory).
Bukaryota: Viridipliantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; Asteridae; euasterids I; Solanales;
Convolvulaceae; Ipomoea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
CHALCONE SYNTHASE B (EC 2.3.1.74) (NARINGENIN-CHALCONE SYNTHASE B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90 VNG-AEKGDVLAVYIESMLPRGVDPYGICAMIPHFGGLTGTDLTAMLNDPLPEK 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82 VGGDPQKGAVLAHHFLEQFHKLSDSFDFCILVAGFGKGTGTGATPVFSKFLSNK 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 92:3338-3342(1995).
                                                                            Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Durbin M.L., Learn G.H., Huttley G.A., Clegg M.T.; "Evolution of the chalcone synthase gene family in the genus
                                                                                                                SEQUENCE FROM N.A.
STRAIN-ATCC 29342 / M129;
MEDLINE; 97105885.
Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P (POTENTIAL).
6C3B531C63F4997E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 98; DB 1; LA Pred. No. 1.14e+00;
          01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
CELL DIVISION PROTEIN FTSZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       396 AA.
                                                                                                                                                                                                             24:4420-4449(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PSO1134; FTSZ_1; 1.
PROSITE; PSO1135; FTSZ_2; 1.
Cell division; Septation; GTP-binding.
NP_BIND 115 GTP (POTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE000051; AAB96167.1; -. PFAM; PF00091; tubulin; 1.
  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             380 AA; 42797 MW;
                                                                                          Mycoplasmataceae; Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 4.18;
Local Similarity 31.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
(Rel. 35, (Rel. 35, (Rel. 35,
                                                                 pneumoniae.
                                                                                                                                                                                                pneumoniae.";
Nucleic Acids Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE; 95241498.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHSB_IPOPU
P48398;
                                                                Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CHS-B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [pomoea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 89123146.
MAKINO S.I., Uchida I., Terakado N., Sasakawa C., Yoshikawa M.;
Makino S.I., Uchida I., Terakado N., Sasakawa C., Yoshikawa M.;
Molecular characterization and protein analysis of the cap region,
which is essential for encapsulation in Bacilius anthracis.";
J. Bacteriol. 171:722-730(1989).
I- FONCTION: ESSENTIAL FOR THE SYNTHESIS OF THE POLYGLUTAMATE
CAPSULE OF BACILLUS ANTHRACIS. MAY FORM A POLYGLUTAMYL SYNTHETASE
COMPLEX TOGETHER WITH CAPA AND CAPC PROTEINS.
TETRAHYDROXYCHALCONE (ALSO TERMED NARINGENIN-CHALCONE OR CHALCONE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UNDER SPECIFIC CONDITIONS SPONTANEOUSLY ISOMERIZE INTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 TIVIV-LIDIWSRRAKRLEGDAKILAIGTATPASWVDQTIYPDFYFRIINSQHLLEHKEK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                              CATALYTIC ACTIVITY: 3 MALONYL-COA + 4-COUMAROYL-COA - 4 COA + NARINGENIN-CHALCONE + 3 CO(2).
PATHWAY: PART OF THE BIOSYNTHETIC PATHWAY FOR ALL CLASSES OF FLAVONOIDS, A LARGE CLASS OF SECONDARY PLANT METABOLITES, MANY OF WHICH ARE BRIGHTLY COLORED.
                                                                                                                                                                                                                                                                                   -!- SIMILARITY: BELONGS TO THE CHALCONE/STILBENE SYNTHASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 98; DB 1; Length 396;
Pred. No. 1.14e+00;
23; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
352C478C1AF892B6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Flavonoid biosynthesis; Transferase; Acyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFAM; PF00195; Chal_stil_synt; 1.
PROSITE; PS00441; CHALCONE_SYNTH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1991 (Rel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43926 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M24150; AAA22286.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U15947; AAC49030.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 4.1%;
Best Local Similarity 23.7%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 297 YMLLSQCGKVRLGNMV 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 FRRICNKSKIRKRHLV 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus anthracis.
Plasmid pTE702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          396 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Multigene family.
ACT_SITE 170
SEQUENCE 396 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAPB PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAPB_BACAN
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                    5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           197 RISEEFLRKFDYMVFP-DNASLALAVAEALGIDEETAFRGMLNAHPD-PGAMRITRFADQ 254
                                                                                                                                                                                                                                                                                           01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR (EC 1.14.99.-).
                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ricinus communis (Castor bean).
Rekaryota, Viridiplantae, Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; Rosidae; eurosids I; Malpighiales;
Euphorbiaceae; Ricinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; L25897; AAA73511.1; -.
PFAM; PF00487; FA_desaturase; 1.
Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane;
                                                                                                                                                                                                                 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OMEGA-3 FATTY ACID DESATURASE.
HISTIDINE BOX 1.
HISTIDINE BOX 2.
HISTIDINE BOX 3.
R36592904EF3C7B0 CRC64;
                                                                                                                                                            Score 99; DB 1; Length 397;
Pred. No. 8.38e-01;
                                                                                                                                                                                                              20; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 98; DB 1; Length 460;
Pred. No. 1.14e+00;
33; Mismatches 48; Indels
                                                                                  POTENTIAL. 7E72A8069DA9D823 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHLOROPLAST (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     460 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-CV. BAKER 296; TISSUE-SEED;
MEDLINE; 94302177.
                                                                                  1 20 Pr
397 AA; 44874 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       460 OM
181 HI
217 HI
384 HI
52561 MW;
HSSP; P14900; 1UAG.
PFAM; PF01225; Mur_ligase; 1.
Transmembrane; Plasmid.
1 FARNSMEM 1 F
                                                                                                                                                               4.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 4.1%;
Best Local Similarity 23.8%;
Matches 29; Conservative
                                                                                                                                                                               Local Similarity 24.68;
les 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    177 1
213 2
380 3
460 AA;
                                                                                                                                                                                                                                                                                                                                                                255 SKPAFFVNG 263
                                                                                                                                                                                                                                                                                                                                                                                                                84 ONGPIMVNG 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transit peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FD3C_RICCO
P48619;
                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
     S FT S
                                                                                                                                                                                                                                                                                                                                                              윱
                                                                                                                                                                                                                                                                                                              ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
```

88 FNGIVNVDEGKGEFFDAGAPPFT-LADIRAAIPKHCWVKNPWRSMSYVLRDVVVVFGLA 146

qq

48; Indels 12;

```
| : | : | | | | | : | | | : | | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 | 326 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             147 AVAAYFNNWVA-WPL-YWFCQGTMF--WALFVLGHDCGHGSFSNNPKLNSVVGHLLHSSI 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         203 LV 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                         ð
```

|| LV 328 327 Search completed: Thu Aug 24 18:51:35 2000 : 27 secs. Job time

* * * *	(TM)
*****	
****	·=====================================
***	<u>''                                  </u>
* * * * * * * * * * * * * * * * * * * *	
* * * * * * * * * * * * * * * * * * * *	
*	
k k k k k	122222

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

Thu Aug 24 18:51:52 2000; MasPar time 26.80 Seconds 848.426 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-214-679-2 (1-328) from US09214679.pep 2417 1 MKWLEESIMAKRGVGAGRKP......GNMVDPKYTVGAMLNKNLLV 328

Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

225878 seqs, 69334122 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

sptrembl12
1:sp\_archea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human
1:sp\_archeate 6:sp\_mammal 7:sp\_mhc 8:sp\_organelle
5:sp\_phage 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified
13:sp\_vertebrate 14:sp\_virus

Mean 47.366; Variance 79.598; scale 0.595 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description	Pred. No.
1	266	11.0	285	. ~	Q9WXX3	ACETAMIDASE, PUTATIVE.	1.52e-32
7	197	8.2	377	Н	Q9YEQ1	377AA LONG HYPOTHETICA	3.16e-18
Э	163	6.7	389	-	058755	389AA LONG HYPOTHETICA	1.19e-11
4	110	4.6	2091	m	P78616	FATTY ACID SYNTHASE, B	1.64e-02
S	109	4.5	789	ഗ	022211	SIMILARITY TO CYTOCHRO	2.34e-02
9	103	4.3	322	~1	067500	POLYSIALIC ACID CAPSUL	1.85e-01
7	103	4.3	393	~	053272	NIFS-LIKE PROTEIN.	1.85e-01
ω	103	4.3	436	10	240118	DELTA-15 LINEOYL DESAT	1.85e-01
6	105	4.3	473	7	Q51454	TRANSCRIPTIONAL ACTIVA	9.38e-02
10	104	4.3	597	S	045218	ALKYL-DIHYDROXYACETONE	1.32e-01
11	104	4.3	1874	~	033765	IGA1 PROTEASE (EC 3.4.	1.32e-01
12	102	4.2	243	ഹ	017308	GABA RECEPTOR SUBUNIT	2.60e-01
13	102	4.2	567	-	026456	SENSORY TRANSDUCTION H	2.60e-01
14	101	4.2	4968	φ	029621	CARDIAC RYANODINE RECE	3.63e-01
15	66	4.1	281	~	030796	MXAE.	7.03e-01
16	98	4.1	387	10	Q9ZTP7	OMEGA-3 FATTY ACID DES	9.75e-01
17	66	4.1	396	10	004970	CHALCONE SYNTHASE (EC	7.03e-01
18	86	4.1	899	٣	059868	CA++-TRANSPORTING ATPA	9.75e-01
19	66	4.1	1056	10	022855	HYPOTHETICAL PROTEIN.	7.03e-01
20	100	4.1	1061	Ŋ	866960	L1156.2 PROTEIN.	5.06e-01

ô

ŏ g RESULT

á

```
Pred. No. 1.19e-11;
17; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                      FATTY ACID SYNTHASE, BETA SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         524 LGVLTNRNKDGT-GVRVILAGSM 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 INSLTPDNHGGNMDVPDIGPGSI 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 33.7%;
les 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01,
08,
           38.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01,
                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY TO CYTOCHROME
                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T05B11.2.
Caenorhabditis elegans.
           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97121482.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-BRISTOL N2;
MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                             LT 4
P78616
P78616;
01-MAY-1997 (
                                                                                                                                     266 NL 267
                                                                                                                                                                        249 QL 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T 5
Q22211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     022211;
                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                   g
                                                               ద
                                                                                                 à
                                                                                                                                                                       á
                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 98344137.

KAWARABAYASI Y., SAWADA M., HORIKAWA H., HAIKAWA Y., HINO Y.,
YAMAMOTO S., SEKINE M., BABA S., KOSUGI H., HOSOYAMA A., NAGAI Y.,
SAKAI M., OGURA K., OTUKA R., NAKAZAWA H., TAKAMIYA M., OHFUKU Y.,
FUNAHASHI T., TANAKA T., KUDOH Y., YAMAZAKI J., KUSHIDA N., OGUCHI A.,
AOKI K., NAKAMURA Y., ROBB T.F., HORIKOSHI K., MASUCHI Y., SHIZUYA H.,
KIKUCHI H.;
220 ACQGDGEICGTAVEFASITTIKVDLIKNWQLSWPRMENAENIMSIGSARPLEDATRIAYR 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146 LGVMGVAPSKELLKEIKEREDRLLKRGGFVLPPTPEGAVPPREPVASEGLRTIPPRENGG 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KAWARABAYSI Y., HINO Y., HORIKAWA H., YAMAZAKI S., HAIKAWA Y., JIN-NO K., TAKAHASHI M., SEKINE M., BABA S., ANKAI A., KOSUGI H., HOSOYAMA A., FUKUI S., NAGAI Y., NISHIJIMA K., NAKAZAWA H., YAKAMIYA M., MASUDA S., FUNAHASHI T., TANAKA T., KUDOH Y., YAMAZAKI J., KUSHIDA N., OGUCHI A., AOKI K., KUBOTA K., NAKAMURA Y., "COMPLETE GENOME SEQUENCE Of an aerobic hyper-thermophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pyrococcus horikoshii.
Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 206 NLDVRHFSPGSKIYFPVFVEGA-LFSVGDAHYAQGDGEVCGTAIEMGATATLRFGVI 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a hyper-
                                     235 ETV-WFIQRRKTIPFTDAYMLASLSVDVGISQLVNPAKTAKARIPKYIF 282
                                                            "Complete sequence and gene organization of the genome of a thermophilic archaebacterium, Pyrococcus horikoshii OT3."; DNA Res. 5:55.76(1998).
EMBL; AD000004.
SEQUENCE 389 AA: 42005 MW; B4D3990F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.2%; Score 197; DB 1; Length 377; larity 34.2%; Pred. No. 3.16e-18; Conservative 27; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 389;
                                                                                                                                        09YE01
09YE01;
01-NOV-1999 (TYEMBLrel. 12, Created)
01-NOV-1999 (TYEMBLrel. 12, Last sequence update)
01-NOV-1999 (TYEMBLrel. 12, Last annotation update)
377AA LONG HYPOTHETICAL ACETAMIDASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           crenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999).
BEQUENCE 377 Aa, 41052 MW; 6FA6B2AE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           389 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last seq
01-JAN-1999 (TrEMBLrel. 09, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                             Archaea; Crenarchaeota; Aeropyrum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1999 (TrEMBLrel, 09, Last
389AA LONG HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                              99310339
                                                                                                                                                                                                                                                                            Aeropyrum pernix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-OT3
                                                                                                                                                                                                                                                                                                                                                                MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JT 3
058755
058755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
```

Matches

g á q δλ RESULT

•

```
4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSET T., COOPER J., COULSON A.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAM J., KIRSTEN J., LAISTER N., LAIREBILLE P.,
LIGHTWING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROPPAR A., SANDIRES D., SHOWNKEEN R.,
SMALDON N., SMITH A., SONNIAMMER E., STADEN R., WATERSTON J.,
THIERRY-MIEG J., THOMAS K., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
                                                                206 GHLDVDSVREGAIVIAPVKVEGGGVYAGDAHAMEGDGEVAGHTTDVTAETTVTVEVIKGL 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   467 IPVYGTKTGDDLRAISDANVVPALVRMITHDP--VNWEQTTAFPNATHIVDFG-PGGISG 523
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BROWN D.W., ADAMS T.H., KELLER N.P., "Aspergillus has distinct fatty acid synthases for primary and secondary metabolism.";
.;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                              Emericella nidulans (Aspergillus nidulans).
Eukaryota; Fungi; Ascomycota; Euascomycetes; Plectomycetes;
Eurotiales; Trichocomaceae; Emericella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 110; DB 3; Length 2091;
Pred. No. 1.64e-02;
15; Mismatches 35; Indels
Indels
                                                                                                                                                                                                                                                                                                             01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. (U.S.A. 93:14873-14877(1996)

EMBL; U75547; AAB41494.1; -.

PFAM; PF00659; Acyl-Lransf; 1.

PFAM; PF01575; MaoC_11ke; 1.

SEQUENCE 2091 AA; 232283 WW; 6B5D181B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Like; 1.
232283 MW; 6B5D181B CRC32;
                                                                                                                                                                                                                                                                         2091 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         789 AA
```

m

```
132 TALREA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 204 PLVRAP 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-H37RV;
                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-H37RV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Limnanthes.
                                                                                                                                                                                                                                                                   MTV012.40C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COLE S.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LT 8
Q40118
Q40118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .eprae."
                                                                                                                         JT 7
053272
                                                                                                                                                                 053272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                       ద
                                                                                                                                              요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HERE REPORTED TO THE REPORT OF THE THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPOR
                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GDMGLLDSKDALI-AISNSGESTEVLYVLQYAKALNIPVIGITGNEKSS-LAKYSDVVLK 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50 GDRIIVDIRDAFEGAINSEQDIPSQLLKMPFLNPQNGPIM-VNGAEKGDVLAVYIESMLP 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  294 IMIDRLQKIET-RICIIASLPITQNTFAACTFIIPNFGFLLIIIKKVILANEL-DKL-MV 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||:: :| : | : |: |: |: |: || 88 IMVNGAEKGDVLAVYIESMLPRGVDPYGICA-MIPHFGGLTGTDLTAMLNDPLPEKVRMI 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L.,
GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER R.,
FELDWAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;
SUDMITTER (JUL.1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AEO00745; AAC07460.1; -.
PFAM; PFO1380; SIS; 1.
SEQUENCE 322 AA; 35114 MW; 677A02DD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ۳.
ک
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
  ij
"2.2 Mb of contiguous nucleotide sequence from chromosome III of elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=VF5;

BEDLINE; 98196666.

BECKERF G. WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L., GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;

"The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               4.5%; Score 109; DB 5; Length 789
6.5%; Pred. No. 2.34e-02;
tive 20; Mismatches 26; Indels
                                                                                                                       GEISEL C., BRADSHAW H.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                         WATERSTON R.;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                  to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 103; DB 2; 1
Pred. No. 1.85e-01;
                                                                                                                                                                                                                                                                                                                                                                          067.1; -.
90761 MW; D7A2F8C9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Aquificales; Aquificaceae; Aquifex,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            322 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LT 6
067500 PRELIMINARY; PRT; 322 AA
067500; 067500; 01-AUG-1998 (TrEMBLrel. 07, Last sequence u)
01-ANG-1998 (TrEMBLrel. 10, Last annotation
POLYSIALIC ACID CAPSULE EXPRESSION PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 4.3%;
Local Similarity 25.2%;
les 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 26.5%;
18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 392:353-358(1998)
                                        Nature 368:32-38(1994)
                                                                                                                                                                                                                                                                                                                                              Submitted (NOV-1996) to EMBL; U53151; AAB37067 SEQUENCE 789 AA; 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                            SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                        STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 351 KMSNLPVF 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         147 KLDSEKVY 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aquifex aeolicus
                                                                                                                                                                                                                                                                                                                             WATERSTON R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-VF5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
```

```
4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE; 9534518.
BHELLA R.S., MACKENZIE S.L.;
"Nucleotide sequence of a CDNA from Limnanthes douglasii L. encoding a delta-15 linoleic acid desaturase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :| :||::| : ||: || | | ||:|| || : ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73 NLAVKGIYWARRDAEPHRRRIVTTEVEHHAVLDSVNWLV-EHEGAHVTWLPTAADGSVSA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "An integrated map of the genome of the tubercle bacillus,
Mycobacterium tuberculosis H37Rv, and comparison with Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=H37RV;
MEDILINE; 96181548.
PHILLIPP W.J., POULET S., EIGIMEIER K., PASCOPELLA L.,
BALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DELTA-15 LINBOYL DESATURASE.
Limnanthes douglasii (Douglas's meadowfoam).
EMRATYOLA; Viridiplantaes, Streptophyta; Ambryophyta; Tracheophyta; euphyllophytes; Spermatophyta, Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Limnanthaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4
                                                                  141 IPVDR-EACP-F-NLAPTVSSTVTLALGDAIAMTLMKLKGFSQEDF-AKRH 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BARRELL B.G., RAJANDREAM M.A., PARKHILL J., COLE S.T.; Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OLIVER K., HARRIS D.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 93:3132-3137(1996).
EMBL, AL021287; CAA1G110.1; -.
PFAM; PF002265; aminotran_5; 1.
SEQUENCE 393 AA; 40947 WW; FED3E34E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.3%; Score 103; DB 2; 1
25.8%; Pred. No. 1.85e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20; Mismatches
                                                                                                                                                                                                                                                                                                                                                393 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   436 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            06,
06,
10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 25.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17; Conservative
                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1998 (TrEMBLrel. 01-JUN-1998 (TrEMBLrel. 01-MAY-1999 (TrEMBLrel. NIFS-LIKE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
```

4

```
033765
                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
       g
                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DI SI DI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
9
                                                                                                                                                                                                                                                                                                                                                                                                  RITCHINGS B.W., ALMIRA E.C., LORY S., RAMPHAL R.;
"Cloning and phenotypic characterization of fles and fles, new
response regulators of Pseudomonas aeruginosa which regulate motility
and adhesion to mucin.";
Infect. Immun. 63:4868-4876(1995).
EMBL: 141213; AAA93330.1; -.
HSSP; P41789; INTR.
PROSITE; PSO00675; SIGMA54_INTERACT_1; 1.
PROSITE; PSO00675; SIGMA54_INTERACT_2; 1.
PROSITE; PSO00688; SIGMA54_INTERACT_2; 1.
PROSITE; PSO00688; SIGMA54_INTERACT_3; 1.
PRAM; PPO00158; sigma54: 11.
SEQUENCE 473 AA; 51264 MW; BA4045A5 CRC32;
                                                                                                                   83 GSPPPF-KLADIRAAIPKHCWVKNQWRSMSYVVRDVVIVLGLAAAAVAANSW-AVWPL-Y 139
                                                                                                                                   DGPVALEPA-SRQLLELAARVARSDSTVLISGESGTGKEVLANYIHQQSPRAGKPFIAIN 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1998 (TrEMBLE-1) 06, Last sequence update)
01-JUN-1999 (TrEMBLE-1) 12, Last annotation update)
ALKYL-DIHYDROXYACETONEPHOSPHATE SYNTHASE (EC 2.5.1.26)
(ALKYLOILYCERONE-PHOSPHATE SYNTHASE)
(ALKYLOILYDROXYACETONEPHOSPHATE SYNTHASE).
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
                                                                                               29; Mismatches 42; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                         Length 436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 473;
                                                                                                                                                                                |: : | | :: | | :: || 284 WLVEDFGFEQWDAYMLLSQCGKVRLGNMVDPKYTVGAMLNKNLLV 328
                                                                                                                                                                 140 WVAQGTMF--WALFVLGHDCGHGSFSNNHKLNSVVGHLLHSSILV 182
                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 105; DB 2; Le
Pred. No. 9.38e-02;
18; Mismatches 21;
                                                                        Score 103; DB 10;
Pred. No. 1.85e-01;
Plant Physiol. 108:861-861(1995).

EMBL: U17063; AAA86690.1; --
MENDEL: 8699; Limdo;1208;8699.

FAMPA: PF00487; FA desaturase; 1.

SEQUENCE 436 AA; 50093 MW; 327D77FE CRC32;
                                                                                                                                                                                                                                       473 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       597 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .T 10
045218 PRELIMINARY; PRT;
045218; (TrEMBLrel. 06, Created)
                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLEEL 01, 01-NOV-1996 (TrEMBLEEL 01, 01-NOV-1999 (TrEMBLEEL 12, TRANSCRIPTIONAL ACTIVATOR.
                                                                       Query Match
4.3%;
Best Local Similarity 22.9%;
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 4.3%;
Local Similarity 30.8%;
Les 20; Conservative
                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                        Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                               STRAIN=PAK;
MEDLINE; 96071911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAAIP 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             || || CAMIP 121
                                                                                                                                                                                                                                   Q51454
Q51454;
Q1-NOV-1996 (
                                                                                                                                                                                                                                                                                                                                              Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117
                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
  RL
DR
DR
SO
                                                                                                                    g
                                                                                                                                           δy
                                                                                                                                                                g
                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δy
```

```
5
                                                                                    MEDLINE; 98113342.

DE VET E.C.J.M., PRINSEN H.C.M.T., VAN DEN BOSCH H.;

"Nucleotide sequence of a cDNA clone encoding a Caenorhabditis elegans homolog of mammalian alkyl-dihydroxyactonephosphate synthase: evolutionary switching of peroxisomal targeting signals.";

Biochem. Biophys. Res. Commun. 242:277-281(1998).

-! CATALYITC ACTIVITY: 1-ACYL-GINCERONE 3-PHOSPHATE + A LONG-CHAIN ALCOHOL = 1-ALKYL-GINCERONE 3-PHOSPHATE + A LONG-CHAIN ACID ANION.

EMBL; AJ002686; CAA05690.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   159 CAIIP-IGG--GTSVTNALDTPETEKRAVISMDMALLDKILWIDRENLTCRAQAGIVGQS 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         399 GGIQSGAIVEPEQVSSLPEYTGPQAGAV-VE-PEQVAPLAEYIGPQAGSVVEPEQVTPL- 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |:|| :||: :| :|| : :| :|| |: :|
63 GAINSEQDI-PSQLLKMP-FINPQNGPIMVNGAEKGDVLAVYIESMLPRGVDPYGICAMI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "A comprehensive genetic study of streptococcal immunoglobulin Al proteases: evidence for recombination within and between species."; EmBL: Y13461; CAA73858.1; -. PRAM; PRO746; Gram_pos_anchor; 1.
PPRAM; PRO746; Gram_pos_anchor; 1.
SEQUENCE: 1874 AA; 208478 MW; 4EF17F74 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus sanguis.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-SK85;
MEDLINE; 98084472.
POULSEN K., REINHOLDT J., JESPERSGAARD C., BOYE K., BROWN T.A., HAUGE M., KILIAN M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 104; DB 2; Length 1874;
Pred. No. 1.32e-01;
21; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.3%; Score 104; DB 5; Length 597;
larity 28.2%; Pred. No. 1.32e-01;
Conservative 25; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
IGA1 PROTEASE (EC 3.4.24.13).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
SEQUENCE FROM N.A.
STRAIN-CB1489 HIM-8(E1489); TISSUE=WHOLE ANIMAL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           597 AA; 66559 MW; AFFB98EE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1874 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174 PEID-SINSLTPDNHGGNMDVPDIG 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 456 PEYTGVQAGSVVSPEQATPLPEYTR 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             216 LERQLNKKGFTCGHEPDSIEFSTLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 29.4%;
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 05, TrEMBLrel. 05, (TrEMBLrel. 08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 12 017308 017308; 01-JAN-1998 (01-JAN-1998 (01-JAN-1998 (01-JAN-1998 (01-NOV-1998 (01-NOV-199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transferase.
SEQUENCE
```

ហ

```
LT 14
Q29621
Q29621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                030796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T 15
030796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                           q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                         33; Indels 13; Gaps 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
ر
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        397 IQAMNASEEAREVLRDAQSRVRAMAILH-ET--IYDSGNFTGVDMGSFITRLIERLVSAY 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GVYG-I-HFR-V-DADVRVNLETAIPLGL-LIN-EA--VTNSIRHAFP-SGE-GSITVTM 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                         19 AQDPSASVDAATGGGSVLGDVNISAILDSFSVSYDK-RVRPNYGGPPVEVGVTMYVLSIS 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMITH D.R., DOUGETTE-STAMM L.A., DELOUGHERY C., LEE H.-M., DUBDIS .
ALDREDGE T., BASHIRZADEH R., BLAKELY D., COOK R., GILBERT K.,
HARRISON D., HOANG L., KEAGLE P., LUMM W., POTHIER B., QIU D.,
SPADAPORA R., VICARE R., WANG Y., WIERZBOWSKI J., GIESON R.,
JIWANI N., CARUSO A., BUSH D., SAFER H., PATWELL D., PRABHAKAR S.,
MACDUGALL S., SHIMER G., GOYAL A., PLETRONSKI S., CHURCH G.M.,
DANIELS C.J., MAO J.-I., RICE P., NOLLING J., REEVE J.N.;
"Complete genome sequence of Methanobacterium thermoautotrophicum
deltaH: functional analysis and comparative genomics.";
J. Bacteriol. 179:7135-7155(1997).
EWBL; AE000821; ABB86621; -.
SEQUENCE 567 AA; 62431 MW; ABFFDD94 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Methanobacterium thermoautotrophicum.
Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55; Indels 15;
                                                                 Eukaryota; Metazoa; Arthropoda; Trachéata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
Cucujiformia; Tenebrionidae; Tribolium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.2%; Score 102; DB 1; Length 567; larity 25.2%; Pred. No. 2.60e-01; Conservative 49; Mismatches 55; Indels 1
                                                                                                                                                                                                                                                                                                                                                               Length 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  138 PLPEKVRM-IKLDSE-KVYWSKRHTLPY-K-PHIGTLSVSPE-IDSI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78 SLSE-VKMDFTLDFYFRQFWTDPR-LAYGKRPGVETLSVGSEFIKNI 122
                                                                                                                                                           SECUENCE FROM N.A.
GLUECK S.B., MACINTYRE R.J.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AR025669; ARB81523.1; -.
PFMA: PF00065; neur_chan; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05, Created)
05, Last sequence update)
07, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ESDGLLYLRVEDDGTGME--GIPDGTVGLSLMRALADQL 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | |:: | :: | |: | |: :||| EIDSINSLTPDNHGGNMDVPDIGPGSITYPLVRAPGGRL 213
                                                                                                                                                                                                                                                                                                                                                            Score 102; DB 5;
Pred. No. 2.60e-01;
                                                                                                                                                                                                                                                                                                          243 AA; 27280 MW; A94921CE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                            28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     267
                                             Tribolium castaneum (Red flour beetle).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SENSORY TRANSDUCTION HISTIDINE KINASE
GABA RECEPTOR SUBUNIT (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                            Query Match 4.2%;
Best Local Similarity 30.8%;
                                                                                                                                                                                                                                                                                                                                                                                                            33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1998 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-DELTA H;
MEDLINE; 98037514.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Methanobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1998
01-AUG-1998
                                                                                                                                                                                                                                                                                      NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LT 13
026456
026456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           175
                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HD DTT ACCOUNTS ACCOU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
```

```
MEDLINE; 98156126.
SPRINGER A.L., AUMAN A.J., LIDSTROM M.E.;
"Sequence and characterization of mxaB, a response regulator involved in regulation of methanol oxidation, and of mxaW, a methanol-regulated gene in Methylobacterium extorquens AMI.";
FEMS Microbiol. Lett. 160:119-124(1998).
EMBL; AF017434; AAC46163.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMA S.;
cardiac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3385 LKEPTPEAEELFRWVAEVFIYWSKSHN--FKREEQNFVVQNEINNMSFLITDTKS-KMSK 3441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

MISSOB-HEART, BRAIN;
MEDILINE; 93147066.

IMAGAWA T., NAKAI J., TAKESHIMA H., NAKASAKI Y., SHIGEKAWA M.;
Expression of Ga(2+)-induced Ga2+ release channel activity from
cardiac ryanodine receptor cDNA in Chinese hamster ovary cells.";
J. Blochem. 112:508-513(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   H.,
the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; alpha subdivision; Methylobacterium.
                                                                                                                                                                                                                                                                               Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 4968;
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-BOMESTIC RABBIT; TISSUE-HEART, BRAIN;
MEDLINE; 910320060.
NAKAI J., IMAGAWA T., HAKAMAT Y., SHIGEKAWA M., TAKESHIMA
"Primary structure and functional expression from cDNA of
ryanodine receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 101; DB 6; Length 496
Pred. No. 3.63e-01;
19; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FDEF5E60 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28758 MW; SC08AFFA CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN*DOMESTIC RABBIT; TISSUE=HEART, BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ¥.
4968 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    281
                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, U50465; AAA93465.1; -. EMBL, U50466; AAA93469.1; -. PFAM; PF01365; RYDR_ITPR; 1. PFAM; PF00622; SPRY; 3. PRINTS; PR0795; RYANODINER. SEQUENCE 4968 AA; 565081 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-NOV-1998 (TrEMBLrel. 08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Methylobacterium extorquens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26.6%;
                                                                                                                                                                                                    CARDIAC RYANODINE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 26.00,
Local 17; Conservative
    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                           01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     281 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3442 AAVS 3445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         194 PDIG 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=AM1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ID DET TO DE DET TO DE TO DET TO DET
```

```
Query Match 4.1%; Score 99; DB 2; Length 281;
Best Local Similarity 25.9%; Pred. No. 7.03e-01;
Matches 21; Conservative 23; Mismatches 33; Indels 4; Gaps
```

184 MPYGVSVSPDGARVFVTNQHA 204 | | | | | | | | | | | | 201 ITYPL-VRAPGGRLFIGDAHA 220

δy qq οχ

Search completed: Thu Aug 24 18:53:01 2000 Job time: 69 secs.